```
Chicken a
Chicken a
Vp3 (apop
HIV TAT t
Maltose b
                                       Human apo
Human apo
                                                      Human apo
Apoptin 1
Chicken a
Chicken a
Chicken a
                                                                                                     Human apo
Human apo
Human apo
Human apo
                                                                                                                                     Chicken a
Human apo
Human apo
                                                                                                                                                                                                                                                                                  Immunogenic peptide; apoptin; cancer; leukaemia; p53; apoptosis; mutein; cytostatic; autoimmune disease; immunosuppressive; VP3; tumour; Bcl-2; gene therapy; hyperplasia; metaplasia; dysplasia; Bcr-abl; mutant; Bcl-2-associating protein; BAG-1; cell proliferation disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells or cancer prone cells, and for treating cancer or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated or recombinant phosphorylated Apoptin (I) also known as VP3 or its functional equivalent and/or its functional fragment. Apoptin induces apoptosis in human malignant and transformed cell lines but not in untransformed cells, by a p53 independent mechanism. Apoptin is therefore a candidate therapeutic for
                      Aam51139 Ram51137 Rade52808 Rade52805 Rade52806 Adm13010 Aau98745
                                                                                                                                    Aau98747 (
Ade52800 F
                                                                             Aau98748
Aau98746
Aau98749
Ade52798
Ade52821
Ade52818
                Aam51138
                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild-type Lys substituted by Arg"
                                                                                                                                                                                                                                                                     Chicken anemia virus synthesised apoptin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Donner
                                                                                                                                                                               ALIGNMENTS
               AAM51138
AAM51139
AAM51139
ADE52803
ADE52805
ADE52806
AAU99746
AAU99746
AAU98748
AAU52288
        AAU98759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ď
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                     Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mumberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 62pp; English
                                                                                                                                                                                                                     AAU98742 standard; peptide; 121
                                                                                                                                                                                                                                                                                                                                                                                                                    19-OCT-2001; 2001WO-NL000771.
                                                                                                                                                                                                                                                                                                                                                                                                                                   20-OCT-2000; 2000EP-00203652
20-OCT-2000; 2000US-0242397P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Noteborn MHM, Rohn JL,
Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-463306/49.
B
                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                    WO200232954-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LEAD-) LEADD
                                                                                                                                                                                                                                                     27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                     25-APR-2002
       Synthetic
                                                                                                                                                                                                                                      AAU98742;
                                                                                                                                                                                                      RESULT 1
                                                                                                                                                                                                              AAU98742
Human apo
Chicken a
VP3 prote
VP3 of ch
                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicken a
Chicken a
Chicken a
Chicken a
TAT-VP3 f
PTD5-VP3
PTD5-VP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAV apopt
CAV hexah
Apoptin-T
Chicken a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIAV prot
Chicken a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAT-GST-V
                                                                                                                                                                                                                                                                                                                                                                                            Chicken a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chicken a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAT-eGFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken a
Apoptin 1
Chicken a
                                                      December 23, 2004, 10:36:00; Search time 155 Seconds (without alignments) 280.040 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                      US-10-083-849B-1
632
1 MNALQEDTPPGPSTVFRPPT.......ESLITTTPSRPRTARRIRL 121
                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                    Aar65201
Aar8849
Aar8849
Aau89750
Aau89750
Abp56095
Abp56095
Abp56096
Abp56097
Abp56097
Abp56097
Abp56097
Abp6097
Abp6097
Abp6097
Abp80975
Aau98756
Aau98756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aau98753
Aay72942
Aay72943
Aag79626
Aau98757
                                                                                                                                                                                                                                                                                                                                                                                            Aau98742
        5.1.6
Compugen Ltd.
                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                              2002273 seqs, 358729299 residues
        GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                           ADM13007
AAR65201
AAR88499
ABP56072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP56096
ABP56094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY72943
AAG79626
                                                                                                                                                                                                                                                                                                                                                                                             AAU98742
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU98752
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU98750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP56092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP56095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP56093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU98755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU98756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY72942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR39984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM13011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU98757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP56097
                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                            geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
                                                                                                                                                                                                                                      A_Geneseq_23Sep04:*
                                                                                                                                                                                                                                               geneseqp1980s:*
geneseqp1990s:*
                                                                                                                                                                                                                                                                                                     geneseqp20048:*
                                                                                                                                                                              length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                    Query
Match
                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                              Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                             Perfect score;
                                                                                                                                                                                                                                       ••
                                                                                                        Sequence:
                                                                                                                                               Searched:
                                                                                                                                                                                                                                      Database
                                                        ä
                                                                                                                                                                                                                                                                                                                                                                    Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                     Run
```

10 PM

```
selective destruction of tumour cells which are resistant to chemotherapeutic agents inducing p53/Bc1-2 associated apoptosis. Also included are a vector comprising a nucleic acid encoding apoptin, (or its functional equivalent and/or its functional fragment) which can be phosphorylating apoptin, a gene delivery vehicle comprising the vector, a concleic acid encoding the vector or vehicle, an anti-apoptin antibody, a nucleic acid encoding the antibody, a vector comprising the antibody a nucleic acid encoding the antibody, a vector comprising the antibody a nucleic acid a host cell comprising the antibody nucleic acid or vector, Apoptin is useful for diagnostic purposes, for detecting the presence of cancer cells or cells that are cancer prone, for detecting the presence of cancer inducing agent, for testing the in vitro treatment effect of apoptin is useful for displaying a tumour specific kinase. Compositions comprising the apoptins and antibodies are useful for treating an individual carrying a disease where enhanced cell compositions comprising the apoptin is observed, e.g. cancer, leukaemia or auto-immune disease. Apoptin is useful as a therapeutic compound for the selective destruction of tumour cells or hyperplasia, metaplasia or dysplasia. Apoptin has no toxic effect in in vivo treatment regimes and induces apoption has no toxic effect in in vivo treatment regimes and induces apoptosis in the absence of functional 153 and cannot be blocked by Bc1-2, Bcr-abl or the Bc1-2-associating protein BAG-1. The present sequence is a synthesised apoptin containing a Lys to Arg mutation at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TADNSESTGFKWVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TADNSESTGFKAVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human, apoptin, NLS; nuclear localisation signal; aberrant-specific apoptosis; cytostatic; immunosuppressive; gene therapy; cell proliferation; cancer; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNALQEDIPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 632; DB 5;
Pred. No. 2.5e-61;
imatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noteborn MHM, Danen-Van Oorschot AAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE52796 standard; peptide; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAR-2003; 2003WO-NL000195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-APR-2002; 2002EP-00076597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-845522/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LEAD-) LEADD BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003089467-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human apoptin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           position 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE52796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       요
```

```
New fragment of Apoptin that induces aberrant-specific apoptosis, useful in preparing a medicament for treating a disease associated with enhanced cell proliferation or decreased cell death, e.g., cancer or autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TADNSESTGFKAVVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "These 5 residues are replaced by Ala-Ala-Ala-Ala-Ala-Ala in a loss-of-function mutant created in the
                                                                                                                             The invention relates to a novel isolated or recombinant fragment of Apoptin that is capable of inducing aberrant-specific apoptosis. A peptide of the invention has cytostatic, and immunosuppressive activity, and may have a use in gene therapy. The fragment of Apoptin, nucleic acid, vector, gene delivery vehicle or host cell is useful in preparing additionant for treating a disease where enhanced cell proliferation or decreased cell death is observed, e.g., cancer or autoimmune disease. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 107. .108 /note= "These 2 residues are replaced by Ala-Ala in a loss-of-function mutant created in the invention"
                                                                                                                                                                                                                                                                                                                                                                                                                1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "This fragment is an inhibitor of an aberrant-
specific Apoptin kinase (tumour-specific kinase)"
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Thr is O-phosphorylated only in malignant or transformed cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour-specific kinase, endogenous substrate, identification,
kinase inhibitor, kinase modulator, cell proliferative disorder,
apoptotic disorder, cancer, autoimmune disease, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                       Length 121;
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAV; tumour-specific phosphorylation;
                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 632; DB 7; Best Local Similarity 100.0%; Pred. No. 2.5e-61; Matches 121; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chicken anaemia virus (CAV) Apoptin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM13007 standard, protein, 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressive; gene therapy.
                                                                                            2; Fig 1; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-2003; 2003WO-NL000294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 106. .110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicken anemia virus,
                                                                                                                                                                                                                                                                                                    Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003089936-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apoptin; VP3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM13007;
                                                          disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
 ####X%X0000000X%
                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
```

```
anaemia virus (CAV) mutant polypeptide(s) - useful as vaccines
                                                                                                                          Chicken anemia virus VP1 protein; apoptosis; cancer therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence corresponds to a VP3 protein from chicken anemia virus, (CAV), and may be used to induce apoptosis directly or to generate antibodies against CAV. The protein may be used as a vaccine or an antitumor agent. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                           antitumor; antibody generation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 3; 53pp; English
                                                                                                                                                                                                                                                                                          94WO-NL000168.
                                                                                                                                                                                                                                                                                                                            93NL-00001272.
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for inducing apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                   Noteborn MHM, Koch G;
                                   (revised)
                                                                                                                                                                               Chicken anemia virus.
                                                                                                                                                                                                                                                                                                                                                                (AESC-) AESCULAAP BV
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-075240/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ82830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 L 121
                                                                                                                                                                                                                  WO9503414-A2
                                                                                                                                                                                                                                                                                          19-JUL-1994;
                                                                                                                                                                                                                                                                                                                            20-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-AUG-2003
15-APR-1996
                                 25-MAR-2003
19-AUG-1995
                                                                                                                                                                                                                                                      02-FEB-1995
                                                                                        7P3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR88499;
AAR65201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR88499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                               The invention relates to a method for identifying a substrate of a kinase capable of phosphorylating Apoptin (also known as VP3) in a manner characteristic of malignant and transformed cells (abbrarate cells).

Confidence apoptosis in malignant and transformed cells, but not in normal cells. This pattern of apoptotic activity is related to the finding that apoptin is phosphorylated on Thr 108 in aberrant cells, whereas it is not phosphorylated on Thr 108 in aberrant cells, whereas it is not phosphorylated at this posttion in normal cells, indicating that there is a tumour-specific kinase activity. The method of the invention aims to identify endogenous cellular substrates for this tumour-specific kinase activity. The method of the invention aims to identify endogenous cellular substrates for this tumour-specific kinase and involves preparing lysates from aberrant and from normal reference cells; incubating the components of the lysates with a molecule capable of recognising phosphorylated Apoptin and phosphorylated substrate of a substrate of a contained using the above method; a method of obtaining a modulator of a kinase involved in aberrant-specific Apoptin phosphorylation; a protein inhibitor of an aberrant-specific Apoptin phosphorylation; a protein inhibitor of an inhibitor; vectors, host cells and gene delivery vehicles comprising the nucell caids; and methods of selecting and identifying a molecule which binds to both aberrant cells but not in normal cells. The tumour-specific kinase substrate identified according to the method of the invention is useful as a drug target. The inhibitor, nucleic acid conciunt to a tumour-specific kinase substrate identified according to the method of a tumour-specific kinase towards its endogenous substrate and cell death is observed, e.g., cancer or autoimmune diseases. The tumour-specific kinase substrate identified according to the method or of the invention is useful as a drug target for these enhanced cell death is observed, e.g., cancer or autoimmune diseases. The 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                        Identifying a substrate of a kinase capable of phosphorylating Apoptin in an aberrant-specific way, useful in inducing apoptosis in tumor cells, comprises preparing aberrant and reference cells and incubating with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 632; DB 7;
100.0%; Pred. No. 2.5e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                      Example; Fig 1; 69pp; English
                19-APR-2002; 2002EP-00076596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 121; Conservative
                                                                                      Noteborn MHM, Rohn JL;
                                                                                                                          WPI; 2003-845561/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                  (LEAD-) LEADD BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apoptin kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
```

ö

```
ô
                                                                                                                      61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRRIR 120
                                                                                                                                      61 TADNSESTGFKNVPDLATDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRRIR 120
                                                           9
                                                                                      9
                                                           1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                             MALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Chicken infectious anaemia virus; vaccination; VP1; VP2; VP3; ss.
Length 121;
                          0; Indels
Score 629; DB 2;
Pred. No. 5.3e-61;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicken anemia virus (usa isolate CIA-1).
                                                                                                                                                                                                                                                                                                                                                                                                  VP3 of chicken infectious anaemia virus.
                                                                                                                                                                                                                                                                                           AAR88499 standard; protein; 121 AA.
 99.28;
                 99.28;
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
            Best Local Similarity 99.2 Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9601116-A1
```

AAR65201 standard; protein; 121 AA.

AAR65201 ID AAR6 XX RESULT 4

```
The present invention describes a fusion molecule (I) comprising at least one protein transduction domain (PTD) and at least one chicken anaemia virus (CAV) VP3 molecule. (I) has cytostatic activity and can be used for inducing cell death. (I) is useful for detecting cancerous or precancerous cells in a mammal. (I) is useful as a magnetic bullet to cancerous cells in a mammal. (I) is useful as a magnetic bullet to selectively kill cancer cells in vitro and in vivo, for inducing cell death, and for preventing or treating cancer and related proliferative disorders. (I) is also useful for studying mechanisms of carcinogenesis and materiases eukaryotic cells. (I) effectively transduces VP3 molecules directly into the cells. (I) attacks cancer and pre-cancerous cells while leaving normal cells relatively unharmed. Since more cells can be targeted by (I) when compared with past attempts using different VP3 constructs, potential for patient relapse and side-effects are greatly reduced. The present sequence represents the CAV VP3 protein sequence which is given in the exemplification of the present invention
                                                                                                                                    Novel fusion molecule useful for preventing or treating cancer, comprises a protein transduction domain and a chicken anemia virus VP3 molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TADNSESTGFKAVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TADNSESTGFKAVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic peptide; apoptin; cancer; leukaemia; p53; apoptosis; mutein; cytostatic; autofimmune disease; immunosuppressive; VP3; tumour; Bc1-2; gene therapy; hyperplasia; metaplasia; dysplasia; Bc1-2; Bc1-2; Bc1-2-associating protein; BAG-1; cell proliferation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.5%; Score 629; DB 6; Length 121; 99.2%; Pred, No. 5.3e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Wild-type Thr substituted by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken anemia virus apoptin T108A mutant.
                                                                                                                                                                                                             Disclosure; Page 22; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU98752 standard; peptide; 121 AA.
                                                Wadia JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alanine scanning; phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 120; Conservative
                                                Ezhevsky SA,
(UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200232954-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                Dowdy SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU98752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU98752
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BXBX1114X88X444X6X6X6X6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The genome of the CIA-1 strain of chicken infectious anaemia virus encodes a VP-1 protein with at least four unique amino acid changes compared to the VP1 protein of other chicken infectious anaemia virus isolates. The new VP1 amino acid sequence exhibits a difference in pathogenic potential and cell tropism as compared to cell culture-adapted strains. New sequences (encoding VP1 (AAT10911), VP2 (AAT10912) and VP3 (AAT10913) and the corresponding polypeptides may be used in strategies to control chicken infectious anaemia such as by vaccination. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                       Chicken infectious anaemia virus strain CIA-1 genome sequences, and novel VP1, sequence - useful to control chicken infectious anaemia such as by vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNALQEDTPPGFSTVPRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cander cell death; cancer; tumour; protein transduction domain; CAV; chicken anaemia virus; cytostatic; proliferative cell disorder; carcinogenesis; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 629; DB 2;
Pred. No. 5.3e-61;
1; Mismatches 0;
                                                                                                                                                                                                           Lucio B, Renshaw R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chicken anaemia virus (CAV) VP3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 43-44; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP56072 standard; protein; 121 AA.
                                                                                                                                                          (CORR ) CORNELL RES FOUND INC
                                             95WO-US008440.
                                                                                         95US-00271094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-APR-2002; 2002WO-US013092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-APR-2001; 2001US-0286099P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                        Schat KA, Soine C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken anemia virus
                                                                                                                                                                                                                                                      WPI; 1996-087514/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                            N-PSDB; AAT10913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 Ľ 121<sup>°</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 1 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200285305-A2
                                      05-JUL-1995;
                                                                                       06-JUL-1994;
                                                                                                               03-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
```

ઠે 유 ò 윱 ò 유 9

Gaps

apoptin; cancer; leukaemia; p53; apoptosis;

Chicken anemia virus apoptin T106A mutant.

(first entry)

27-AUG-2002

AAU98750;

```
The invention relates to an isolated or recombinant phosphorylated

Apoptin (I) also known as VP3 or its functional equivalent and/or its

functional fragment. Apoptin in induces apoptosis in human malignant and

transformed cell lines but not in untransformed cells, by a p52

independent mechanism. Apoptin is therefore a candidate therapeutic for

selective destruction of tumour cells which are resistant to

chemotherapeutic agents inducing p53/P61-2 associated apoptosis. Also

concluded are a vector comprising a nucleic acid encoding apoptin, (or its

functional equivalent and/or its functional fragment) which can be

thosphorylating apoptin, a gene delivery vehicle comprising the vector.

CC functional equivalent entibody, a vector comprising the vector, a

cc nucleic acid encoding the antibody a vector comprising the presence of

thosphorylating apoptin, a gene delivery vehicle comprising the presence of

concernication and for diagnostic purposes, for detecting the presence of

cancer cells or cells comprising the antibody nucleic acid or vector,

Apoptin is useful for diagnostic purposes, for detecting the presence of

cancer cells or cells that are cancer prone, for identifying a putative

cancer-inducing agent, for testing the in vitro treatment effect of

apoptin on tumour cells, and for identifying a tumour specific kinase.

CC mopositions comprising the apoptins and antibodies are useful for

treating an individual carrying a disease where enhanced cell

cr auto-immune disease. Apoptin is useful as a therapeutic compound for

treating an individual carrying adisease where enhanced cell

cr auto-immune disease. Apoptin is useful as a therapeutic compound for

the selective destruction of tumour cells or hyperplasia, metaplasia or

cyapplasia. Apoptin has no toxic effect in in vivo treatment regimes and

conducted apoptosis in the absence of functional p53 and cannot be blocked

conducted to the selective destruction of tendent processed the present enhanced cell processed to the selective destruction 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence is an apoptin mutant created during an alanine scanning experiment for mapping the phosphorylation sites in apoptin. Note: The present sequence is not shown in the specification but was created by the indexer using the information in figure 4 and the wild-type apoptin
                                                                                                                                                                                                                                                                                                                                         Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells or cancer prone cells, and for treating cancer or autoimmune disease.
                                                                                                                                                                                                                              Donner P;
                                                                                                                                                                                                                              ď
                                                                                                                                                                                                                              Mumberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page; 62pp; English.
                             19-OCT-2001; 2001WO-NL000771.
                                                                                   20-OCT-2000; 2000BP-00203652.
20-OCT-2000; 2000US-0242397P.
                                                                                                                                                                                                                              Rohn JL,
                                                                                                                                                                                                                                                                                      WPI; 2002-463306/49.
                                                                                                                                                                      (LEAD-) LEADD BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein sequence
                                                                                                                                                                                                                              Noteborn MHM,
```

```
TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSBYRVSELKESLITTTPSRPRTARRRIR 120
                                                                                                                                            61 TADNSESTGFKAVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRPRTAKRRIR 120
                                                                                 1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITILSLCGCANARAPILESA 60
                                                             1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                  Gaps
                                 ö
   Length 121;
                               1; Indels
Score 624; DB 5;
Pred. No. 1.9e-60;
1; Mismatches 1;
98.7%;
                             Matches 119; Conservative
              Local Similarity
                                                                                                                                                                                          121 1, 121
                                                                                                                                                                                                                          i 121
                                                                                                                             61
Query Match
                                                                                          셤
                                                                                                                            δ
                                                                                                                                                           셤
                                                                                                                                                                                          8
                                                                                                                                                                                                                        셤
```

Sequence 121 AA;

Sequence 121 AA

AAU98750 standard; peptide; 121 AA.

AAU98750 ID AAU9 XX RESULT 8

```
sequence is an apoptin mutant created during an alanine scanning experiment for mapping the phosphorylation sites in apoptin. Note: The present sequence is not shown in the specification but was created by the indexer using the information in figure 4 and the wild-type apoptin.
                                                                                                                                                                                                                                                                                   Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells or cancer prone cells, and for treating cancer or autoimmune disease.
                                                      cytostatic; autoimmune disease; immunosuppressive; VP3; tumour; Bc1-2; gene therapy; hyperplasia; metaplasia; dysplasia; Bcr-abl; mutant; Bc1-2-associating protein; BAG-1; cell proliferation disorder;
                                                                                                                                        /note= "Wild-type Thr substituted by Ala"
                                                                                                                                                                                                                                                   Donner P;
                                                                                                                                                                                                                                                   Mumberg D,
                                                                                                                .
Misc-difference 106
                                                                                 alanine scanning; phosphorylation.
                                                                                                                                                                                                                                                                                                                    Disclosure; Page; 62pp; English.
                                                                                                                                                                                          19-OCT-2001; 2001WO-NL000771.
                                                                                                                                                                                                          20-OCT-2000; 2000EP-00203652.
20-OCT-2000; 2000US-0242397P.
                                                                                                                                                                                                                                                   Noteborn MHM, Rohn JL,
                                                                                                Chicken anemia virus.
                                               Immunogenic peptide;
                                                                                                                                                                                                                                                                   WPI; 2002-463306/49.
                                                                                                                                                                                                                                   (LEAD-) LEADD BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein sequence
                                                                                                                                                         WO200232954-A2
                                                                                                                                                                         25-APR-2002.
                                                                                                          Synthetic.
```

```
concein comprising the vector or vehicle, an anti-apoptin antibody, a nucleic acid encoding the antibody, a vector comprising the antibody nucleic acid, a host cell comprising the antibody nucleic acid, a host cell comprising the antibody nucleic acid or vector, Apoptin is useful for diagnostic purposes, for detecting the presence of cancer inducing agent, for testing the in vitro treatment effect of apoptin on tumour cells, and for identifying a tumour specific kinase. Compositions comprising the apoptins and antibodies are useful for treating an individual carrying a disease where enhanced cell corrected or auto-immune disease. Apoptin is useful as a therapeutic compound for the selective destruction of tumour cells or hyperplasia, metaplasia or dysplasia. Apoptin has no toxic effect in in vivo treatment regimes and induces apoption the absence of functional p53 and cannot be blocked by Bcl-2, Bcr-abl or the Bcl-2-associating protein BAG-1. The present sequence is an apoptin mutant created during an alanine scanning experiment for mapping the phosphorylation sites in apoptin. Note: The present sequence is not shown in the specification but was created by the indexer using the information in figure 4 and the wild-type apoptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel fusion molecule useful for preventing or treating cancer, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TADNSESTGFKOVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITATPSRPRTAKRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cancer cell death, cancer; tumour; protein transduction domain; CAV; chicken anaemia virus; cytostatic; proliferative cell disorder; carcinogenesis; metastasis; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 624; DB 5; Length 121; Pred. No. 1.9e-60; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP56092 standard; protein; 190 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wadia JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                          98.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-2002; 2002WO-US013092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-2001; 2001US-0286099P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 98.3
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dowdy SF, Ezhevsky SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAT-VP3 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicken anemia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-093056/08.
N-PSDB; ABZ21714.
                                                                                                                                                                                                                                                                                                                                                                       protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200285305-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP56092;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
ABP56092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated or recombinant phosphorylated Apoptin (1) also known as VP3 or its functional equivalent and/or its functional fragment. Apoptin induces apoptosis in human malignant and transformed cell lines but not in untransformed cells, by a p53 independent mechanism. Apoptin is therefore a candidate therapeutic for selective destruction of tumour cells which are resistant to chemocherapeutic agents inducing p53/Bcl-2 associated apoptosis. Also included are a vector comprising a nucleic acid encoding apoptin, (or its functional equivalent and/or its functional fragment) which can be phosphorylated and a nucleic acid encoding a kinase capable of phosphorylating apoptin, a gene delivery vehicle comprising the vector, a
                                                                                                                                                                                                  TADNSESTGFKAVPDLRTDOPKPSKKRSCDPSBYRVSELKESLIATTPSRPRTAKRRIR 120
                                                                                                                                                                               61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                       9
                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic peptide, apoptin; cancer; leukaemia; p53; apoptosis; mutein; cytostatic; autoimmune disease; immunosuppressive; VP3; tumour; Bcl-2; gene therapy; hyperplasia; metaplasia; dysplasia; Bcr-abl; mutant; Bcl-2-associating protein; BGC-1; cell proliferation disorder; alanine scanning; phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated or recombinant phosphorylated Apoptin or its functional equivalent or fragment, useful for detecting presence of cancer cells or cancer prone cells, and for treating cancer or autoimmune disease.
                                                                                                                          1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                       1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                  Gaps
                                                                  ö
                           Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Wild-type Thr substituted by Ala"
                                                                  1; Indels
                             Score 624; DB 5;
Pred. No. 1.9e-60;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Donner P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken anemia virus apoptin T107A mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     AAU98751 standard; peptide; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mumberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page, 62pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-OCT-2001; 2001WO-NL000771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-OCT-2000; 2000EP-00203652,
20-OCT-2000; 2000US-0242397P,
                             98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rohn JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-463306/49.
                           Query Match
Best Lócal Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LEAD-) LEADD BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200232954-A2
                                                                                                                                                                                                                                                       L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noteborn MHM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                          AAU98751;
                                                                                                                                                                                                                                                                                                                                                                  AAU98751
                                                                                                                                                                                                                윱
                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                               ò
                                                                                                                                                                                                                                                         ઠે
```

Gaps

```
The present invention describes a fusion molecule (I) comprising at least one protein transduction domain (PTD) and at least one chicken anaemia virus (CAV) vP3 molecule. (I) has cytostatic activity and can be used for inducing cell death. (I) is useful if or detecting cancerous or precancerous cells in a mammal. (I) is useful as a magnetic bullat to cancerous cells in a mammal. (I) is useful as a magnetic bullat to cancerous or preventing or treating cancer and related proliferative death, and for preventing or treating cancer and related proliferative disorders. (I) is also useful for studying mechanisms of carcinogenesis and metastases eukaryotic cells. (I) effectively transduces VP3 molecules directly into the cells. (I) attacks cancer and pre-cancerous cells while leaving normal cells relatively unharmed. Since more cells can be cargeted by (I) when compared with past attempts using different VP3 constructs, potential for patient relapse and side-effects are greatly concerned. The present sequence represents a TAT-VP3 fusion protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 NALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSAT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel fusion molecule useful for preventing or treating cancer, comprises a protein transduction domain and a chicken anemia virus VP3 molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a fusion molecule (I) comprising at least
a protein transduction domain and a chicken anemia virus VP3 molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NALOEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cancer cell death, cancer, tumour, protein transduction domain, CAV, chicken anaemia virus, cytostatic, proliferative cell disorder; carcinogenesis, metastasis, fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 624; DB 6;
Pred. No. 3.3e-60;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP56095 standard; protein; 190 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wadia JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 36; Fig 5B; 104pp; English.
                                    Claim 36; Fig 2; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-APR-2002; 2002WO-US013092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-2001; 2001US-0286099P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTD4-VP3 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dowdy SF, Ezhevsky SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                    the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken anemia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-093056/08
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200285305-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP56095;
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
```

```
cone protein transduction domain (PTD) and at least one chicken anaemia virus (CAV) VP3 molecule. (1) has cytostatic activity and can be used for inducing cell death. (1) is useful for detecting cancerous or precancerous cells in a mammal or for killing or injuring cancerous or precancerous cells in a mammal. (1) is useful as a magnetic bullet to cancerous cells in a mammal. (1) is useful as a magnetic bullet to cancerous cells in a mammal. (1) is useful as a magnetic bullet to cancerous cells in vitro and in vivo, for inducing cell death, and for preventing or treating cancer and related proliferative disorders. (1) is also useful for studying mechanisms of carcinogenesis can metastasses eukaryotic cells. (1) effectively transduces VP3 molecules directly into the cells. (1) attacks cancer and pre-cancerous cells while carried normal cells relatively unharmed. Since more cells can be carried to many compared with past attempts using different VP3 constructs, potential for patient relapse and side-effects are greatly reduced. The present sequence represents a PTD4-VP3 fusion protein from
                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 ADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIRL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a fusion molecule (I) comprising at least one protein transduction domain (PTD) and at least one chicken anaemia virus (CAV) VP3 molecule. (I) has cytostatic activity and can be used for inducing cell death. (I) is useful for detecting cancerous or precancerous cells in a mammal or for killing or injuring cancerous or precancerous cells in a mammal. (I) is useful as a magnetic bullet to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel fusion molecule useful for preventing or treating cancer, comprises a protein transduction domain and a chicken anemia virus VP3 molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer cell death; cancer; tumour; protein transduction domain; chicken anaemia virus; cytostatic; proliferative cell disorder; carcinogenesis; metastasis; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                Score 624; DB 6; Length 190;
Pred. No. 3.3e-60;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP56096 standard; protein; 190 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wadia JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim, 36, Fig 5C; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-2001; 2001US-0286099P.
                                                                                                                                                                                                                                                                                                                                                                y Match 98.7%;
Local Similarity 99.2%;
les 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-2002; 2002WO-US013092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTD5-VP3 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ezhevsky SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-093056/08
                                                                                                                                                                                                                                                                                                                               Sequence 190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200285305-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dowdy SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP56096;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
ABP56096
ID ABP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
selectively kill cancer cells in vitro and in vivo, for inducing cell death, and for preventing or treating cancer and related proliferative disorders. (I) is also useful for studying mechanisms of carcinogenesis and metaetresses eukaryotic cells. (I) effectively transduces VP3 molecules directly into the cells. (I) attacks cancer and pre-cancerous cells while leaving normal cells relatively unharmed. Since more cells can be targeted by (I) when compared with past attempts using different VP3 constructs, potential for patient relapse and side-effects are greatly reduced. The present sequence represents a PTD5-VP3 fusion protein from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIRL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 624; DB 6; L
Pred. No. 3.3e-60;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.2
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                    8 \pm 8 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      용
```

ABP56094 standard; protein; 190 AA (first entry) PTD3-VP3 fusion protein. 27-FEB-2003 ABP56094; RESULT 13 

chicken anaemia virus; cytostatic; protein transduction domain; CAV; carcinogenesis; metastasis; fusion protein. Chicken anemia virus. Synthetic.

WO200285305-A2.

31-OCT-2002

24-APR-2002; 2002WO-US013092

(UNIW ) UNIV WASHINGTON

24-APR-2001; 2001US-0286099P

Wadia JS; Ezhevsky SA, Dowdy SF,

WPI; 2003-093056/08

Novel fusion molecule useful for preventing or treating cancer, comprises a protein transduction domain and a chicken anemia virus VP3 molecule.

Claim 36; Fig 5A; 104pp; English.

The present invention describes a fusion molecule (1) comprising at least one protein transduction domain (PTD) and at least one chicken anaemia virus (CAV) VP3 molecule. (1) has extostatic activity and can be used for inducing call death. (1) is useful for detecting cancerous or precancerous cells in a mammal. (1) is useful as a magnetic bullet to selectively kill cancer cells in virto and in vivo, for inducing call death, and for preventing or treating cancer and related proliferative disorders. (1) is also useful for studying mechanisms of carcinogenesis and metastases eukaryotic cells. (1) effectively transduces VP3 molecules directly into the cells. (1) attacks cancer and pre-cancerous cells while

```
The present invention describes a fusion molecule (I) comprising at least one protein transduction domain (PTD) and at least one chicken anaemia cone protein transduction domain (PTD) and at least one chicken anaemia control of the concerous cells in a mammal. (I) is useful for detecting cancerous or precancerous cells in a mammal. (I) is useful as a magnetic bullet to cancerous cells in a mammal. (I) is useful as a magnetic bullet to selectively kill cancer cells in vitro and in vivo, for inducing cell death, and for preventing or treating cancer and related proliferative clisciders. (I) is also useful for studying mechanisms of carcinogenesis and metastases eukaryotic cells. (I) effectively transduces VP3 molecules directly into the cells. (I) attacks cancer and pre-cancerous cells while targeted by (I) when compared with past attempts using different VP3 constructs, potential for patient relapse and side-effects are greatly reduced. The present sequence represents a TAT-GST-VP3 fusion protein
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                         130
                                                                                                                                                                                                                                                                                              62 ADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIRL 121
                                                                                                                                                                                                                                                                                                                 Novel fusion molecule useful for preventing or treating cancer, comprises a protein transduction domain and a chicken anemia virus VP3 molecule.
                                                                                                                                                                                                                        61
leaving normal cells relatively unharmed. Since more cells can be targeted by (1) when compared with past attempts using different VP3 constructs, potential for patient relapse and side-effects are greatly reduced. The present sequence represents a PTD3-VP3 fusion protein from
                                                                                                                                                                                                                                            2 NALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cancer cell death; cancer; tumour; protein transduction domain; chicken anaemia virus; cytostatic; proliferative cell disorder; carcinogenesis; metastasis; fusion protein.
                                                                                                                                                                                     .;
0
                                                                                                                                               Score 624; DB 6; Length 190;
Pred. No. 3.3e-60;
                                                                                                                                                                                    0; Indels
                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Fig 18A-D; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                ABP56097 standard; protein; 422 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wadia JS;
                                                                                                                                               98.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-APR-2002; 2002WO-US013092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-APR-2001; 2001US-0286099P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAT-GST-VP3 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                     Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ezhevsky SA,
                                                                             the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-093056/08.
                                                                                                                                                   Query Match.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABZ21716
                                                                                                              Sequence 190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200285305-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dowdy SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP56097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 88888888
                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                    à
```

ઠે 셤 ઠે

```
Search completed: December 23, 2004, 11:00:10 Job time : 157 secs
                                                                                                         g
                                                                                                                                               ઠે
                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a fusion molecule (I) comprising at least one protein transduction domain (PTD) and at least one chicken anaemia virus (CAV) VP3 molecule. (I) has cyrostatic activity and can be used for inducing cell death. (I) is useful for detecting cancerous or precancerous cells in a mammal. (I) is useful as a magnetic bullet to cancerous cells in a mammal. (I) is useful as a magnetic bullet to selectively kill cancer cells in virus and in vivo, for inducing cell death, and for preventing or treating cancer and related proliferative disorders. (I) is also useful for studying mechanisms of carcinogenesis and materatesse sukaryotic cells. (I) effectively transduces VP3 molecules directly into the cells. (I) attacks cancer and pre-cancerous cells while leaving normal cells relatively unharmed. Since more cells can be transdeed by (I) when compared with past attempts using different VP3 reduced. The present sequence represents a TAT-eGFP-VP3 fusion protein contructs, potention
                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel fusion molecule useful for preventing or treating cancer, comprises a protein transduction domain and a chicken anemia virus VP3 molecule.
                                                                                                                                                                                303 NALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSAT 362
                                                                                                                                                                                                               ADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIRL 121
                                                                                                                                                                                                                                     363 ADNSESTGFKAVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRRIRL 422
                                                                                                                                               61
                                                                                                                                               2 NALOEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSAT
                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer cell death; cancer; tumour; protein transduction domain; CAV; chicken anaemia virus; cytostatic; proliferative cell disorder; carcinogenesis; metastasis; fusion protein.
                                                                         Length 422;
                                                                                                           0; Indels
                                                                       Score 624; DB 6;
Pred. No. 8.6e-60;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                             ABP56093 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wadia JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 36; Fig 4; 104pp; English.
                                                                   Query Match
Best Local Similarity 99.2%;
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-2002; 2002WO-US013092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-APR-2001; 2001US-0286099P
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAT-eGFP-VP3 fusion protein.
from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dowdy SF, Ezhevsky SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chicken anemia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-093056/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABZ21715.
                                   Sequence 422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200285305-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                  ABP56093;
                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                                                                ABP56093
SXS
                                                                                                                                                                                                                                                  a
```

:

Seguence 432 AA;

```
ö
                                                                              2 NALOEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSAT
                                 Gaps
                                 ö
 98.7%; Score 624; DB 6; Length 432; 99.2%; Pred. No. 8.8e-60; Indels iive 1; Mismatches 0; Indels
Query Match
Best Local Similarity 99.2
Matches 119; Conservative
```

This Page Blank (uspto)

```
USA
                                                                                                                                                                                                                                                                                                                                                   US-08-489-666C-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
STATE:
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 25918, A
Sequence 2551, A
Sequence 24227, A
Sequence 41118, A
Sequence 41118, A
Sequence 41118, A
Sequence 4118, A
Sequence 2934, A
Sequence 2934, A
Sequence 2938, A
Sequence 2938, A
Sequence 2267, A
Sequence 2267, A
Sequence 2267, A
Sequence 2267, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31, Appl
59394, A
43987, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                             (without alignments)
211.170 Million cell updates/sec
                                                                                                                                                      US-10-083-849B-1
632
1 MNALQEDTPPGPSTVFRPPT......BSLITTTPSRFRTARRIRL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                               December 23, 2004, 10:53:21 ; Search time 38 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-489-666C-7

US-08-911-092-7

US-08-484-121A-7

US-08-484-121A-7

US-08-484-121A-7

US-09-057-963A-6

US-09-252-991A-2591B

US-09-252-991A-2591B

US-09-252-991A-2762B

US-09-252-991A-2762B

US-09-252-991A-2762B

US-09-252-991A-2762B

US-09-252-991A-2762B

US-09-252-991A-2762B

US-09-270-767-46140

US-09-270-767-46140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-252-991A-29008
-09-252-991A-18940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-252-991A-29008
US-09-252-991A-18940
US-09-252-991A-23167
                                                                                                                                                                                                                                                                                     Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                           478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                             Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                         Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                 Post-processing:
                                                                                                                                                       Title:
Perfect score;
Sequence:
                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           629
629
629
629
629
629
86.5
87.5
81.5
81.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.5
78.5
78.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.5
76.5
74.5
74.5
                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                           Searched:
                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
No.
```

```
28 74 11.7 195 4 10.99-252-905.

29 74 11.7 195 4 10.99-252-905.

20 74 11.7 491 1 10.99-90-252-905.

20 74 11.7 491 1 10.99-90-290.

21 11.7 491 1 10.99-90-290.

22 74 11.7 491 1 10.99-90-10.99-90-10.

23 74 11.7 491 1 10.99-90-10.99-90-10.

24 11.7 491 1 10.99-90-10.99-90-10.

25 74 11.7 491 1 10.99-90-10.99-90-10.

26 74 11.7 491 1 10.99-90-10.99-90-10.

27 74 11.7 491 1 10.99-90-10.99-90-10.

28 74 11.7 491 1 10.99-90-10.99-90-10.

28 74 11.7 491 1 10.99-90-10.99-90-10.

29 74 11.7 491 1 10.99-90-10.90-90-10.

20 74 11.7 491 1 10.99-90-10.90-90-10.

20 74 11.7 491 1 10.99-90-10.90-90-10.

20 74 11.7 491 1 10.99-90-10.90-90-10.

20 74 11.7 491 1 10.99-90-10.90-90-10.

20 74 11.7 491 1 10.99-90-10.90-90-10.

20 74 11.7 491 1 10.99-90-10.90-90-10.

20 74 11.7 491 1 10.99-90-10.90-10.

21 74 11.7 491 1 10.99-90-10.90-10.90-90-10.

22 74 11.7 491 1 10.99-90-10.90-10.90-90-10.

23 74 11.7 491 1 10.99-90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.90-10.
```

```
61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TADNSESTGFKAVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 629; DB 2; Length 121;
Pred. No. 9.8e-66;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08485001B
Patent No. 5981502
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Koch, Guus
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
TITLE OF INVENTION: APOPTOSIS IN TUMOR CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLICATION NUMBER: US/08/485,001B
FILLIGATION DATE: 07-UUNE-1995
            PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9002008
FILING DATE: 12-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter: Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: LEBV003.00US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4407
TELEPHONE: (650) 328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Rae-Venter Law Group, P.C. STREET: P.O. Box 60039
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-JUNE 1995
CLASCHTCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/454,121
FILING DATE: 30-NOVEMBER-1995
FRICK APPLICATION DATA:
APPLICATION NUMBER: PCT/NL94/00168
FILING DATE: 19-JULY-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/030,335
PRIOR APPLICATION DATA: B-MARCH-1993
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: NL 9301272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.5%;
Best Local Similarity 99.2%;
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 L 121
                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-08-485-001B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-911-092-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08911092
Sequence 7, Application US/08911092
Sequence 7, Application US/08911092
Sequence No. 5952002
GENERAL INFORMATION:
APPLICANT: NO. 5952002eborn, Matheus H.M.
APPLICANT: NO. 5952002eborn, Matheus H.M.
APPLICANT: NOCCH, Guus
TITLE OF INVENTION: Chicken Anemia Virus Mutants And Vaccines
TITLE OF INVENTION: Sequences Of That Virus Coding Therefor
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Rea-Venter Law Group, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TADNSESTGFKOVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTPSRPRTAKRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                             1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                            Length 121;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: BA306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE Floppy disk
COMPUTER: BA FOLICATION
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/911,092
FILING DATE: 14-A06-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/454,121
FILING DATE: 30-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PT/NL94/00168
FILING DATE: 19-UULY-1994
RAPPLICATION NUMBER: NL 9301272
FILING APPLICATION NUMBER: US 08/030,335
FILING DATE: 20-UULY-1993
RAPPLICATION NUMBER: US 08/030,335
FILING DATE: 8-MAR-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/NL91/00165
FILING DATE: 11-SEP-1991
                                                                                                                                                                                                                                                                                                                  99.5%; Score 629; DB 2; Lv 99.2%; Pred. No. 9.8e-66; iive 1; Mismatches 0;
TELEFAX: (650)320-7.
TELEX: N/A
; INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
; LENGTH 121 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
: STRANDENESS: unknown
: TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.O. Box 60039
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 99.2
Matches 120; Conservative
                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 L 121
                                                                                                                                                                                                                                                                    US-08-489-666C-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-911-092-7
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

Gaps

```
US-WAZ-LOLD-7

US-WAZ-LOLD-7

Sequence 7, Application US/08482161B

Patent No. 6162461

GENERAL INFORMATION:

APPLICANT: No. 6164461eborn, Matheus H.M.

APPLICANTON: Sequences Of That Virus Coding Therefor

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS: 40039

CITY: Palo Alto

STATE: California

COUNTRY: USA

COMPUTER: EM PC compatible

COMPUTER: EM PC compatible

COMPUTER: EM PC compatible

COMPUTER: Datentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/482,161B

FILING DATE: 07-UUNE-1995

CLASSIFICATION NUMBER: US 08/454,121

PRIOR APPLICATION NUMBER: US 08/454,121

PRIOR APPLICATION NUMBER: US 08/454,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 629; DB 3; Length 121;
Pred. No. 9.8e-66;
1; Mismatches 0; Indels
                  PILING DATE: 8-MAR-1993
PRIOR APPLICATION NUMBER: US 08/030,335
PRIOR APPLICATION NUMBER: PT/NL91/00165
PILING DATE: 11-SEP-1991
PRIOR APPLICATION NUMBER: NL 9002008
PILING DATE: 11-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 12,750
REFERENCE/DOCKET NUMBER: LEBV.003.00US
TELEPHONE: (650) 328-4470
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERICATION:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.2%;
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 121 amino acids
TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MOLECULE TYPE: protein
) HYPOTHETICAL: NO
US-08-454-121A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-482-161B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08454121A
Patent No. 6071520
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE:
CORRESPONDENCE:
ADDRESSE:
ROUTH OF INVENTION:
Sequences Of That Virus Coding Therefor
CORRESPONDENCE:
ADDRESSE:
ROUTH OF INVENTION:
SEQUENCE:
ADDRESSE:
ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,121A
PILNG DATE: 07-JUNE-1995
PLING APPLICATION 1435
PRIOR APPLICATION NUMBER: PCT/NL94/00168
FILING DATE: 19-JULY-1994
PRIOR APPLICATION NUMBER: RT/NL94
PRIOR APPLICATION NUMBER: NL 9301272
FILING DATE: 20-JULY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 629; DB 2;
Pred. No. 9.8e-66;
                                                                                                                                                                                                                                                                     NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: LEBV.003.02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 926-6205
TELEPRAX: (650) 424-8760
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acide
TYPE: amino acide
TYPE: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL91/00165
FILING DATE: 11-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N. 9002008
FILING DATE: 12-SEPTEMBER-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.5%;
ilarity 99.2%;
Conservative
20-JULY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: P.O. Box 60
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 120; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-485-001B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-454-121A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

ö

Gaps

```
Sequence 25918, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT PILITING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-18
PRIOR PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TADNSESTGFKAVVPDLRTDQPKPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPILRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.5%; Score 629; DB 3; Length 121; 99.2%; Pred. No. 9.8e-66; Live 1; Mismatches 0; Indels
                                                                                                                                  PELLICATION NUMBER: US 08/454,121

PRICIA APPLICATION DATA:
APPLICATION NUMBER: US 08/030,335

FILING DATE: 08-MAR-1993

PRIOR APPLICATION NUMBER: US 08/030,335

FILING DATE: 19-JUJ-1994

PRIOR APPLICATION NUMBER: PCT/NL 94/00168

FILING DATE: 19-JUJ-1994

PRIOR APPLICATION NUMBER: PCT/NL 91/00165

FILING DATE: 11-5EP-1991

PRIOR APPLICATION NUMBER: NL 9301272

FILING DATE: 20-JUJ-1993

PRIOR APPLICATION NUMBER: NL 9002008

FILING DATE: 12-SEP-1990

ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA

REGISTRATION NUMBER: LEBV.003.04US

TELECOMUNINICATION NUMBER: LEBV.
                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/489,666
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/454,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (650)328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: N/A
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.2
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (650) 328-4477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-252-991A-25918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-057-963A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chicken Anemia Virus mutants and vaccines and uses based on the viral proteins VP1, VP2 and VP3 or sequences of that virus coding therefor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TADNSESTGFKNVPDLRIDOPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.5%; Score 629, DB 3; Length 121; Best Local Similarity 99.2%; Pred. No. 9.8e-66; Matches 120; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PLING DATE: US/09/057,963A PILLING DATE: 09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                           NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: LEBV.003.01US
             FILING DATE: 19-JULY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/030,335
FILING DATE: 08-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NL 9301272
FILING DATE: 20-JULY-1993
PRIOR APPLICATION DATA:
FILING DATE: 20-JULY-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA: NL 9002008
FILING DATE: 11-SEPTEMBER-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEE: RAE-VENTER LAW GROUP, P.C.
T: P.O. BOX 60039
PALO ALTO
APPLICATION NUMBER: PCT/NL 94/00168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: No. 6217870eborn, M.H.M
APPLICANT: Koch, G.
TITLE OF INVENTION: Chicken Anemia Vi
TITLE OF INVENTION: vaccines and uses
TITLE OF INVENTION: vp3 or sequences
TITLE OF INVENTION: VP3 or sequences
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-057-963A-6; Sequence 6, Application US/09057963A; Patent No. 6217870; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (650) 926-6205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 424-8760
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 121 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 i 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-482-161B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
```

à

à g ઠે a

```
ద
                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                     ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30531, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                  55 ---PILRSATADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TADNSEST------GFKNVPDLRTDQPKPP-SKKRSCDPSEYRVSELKESLITTTPSR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----RLWHRGPAH 481
                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 PPGPSTVFRPPTSSRPLETPHCREIRIGIAGITIT-----LSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PP-----PPTSS-----ARARKVRVGTPGIRPNSTSNRPPISSALGCATTCSPMSLPR 48
                                                                                                                                                                                                                      9 PPGPSTVFRPPTS-SRPLETP------HCREIRIGIAGITITLSLCGCANARA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Indels 34; Gaps
                                                                                                                               13.7%; Score 86.5; DB 4; Length 757; 27.9%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 488;
                                                                                                                                                                             53; Indels
                                                                                                                                                                                                                                                                                                                                                     432 GRRPGORSGSRRRPARPRRAPGPPRRTDOGOPRLHROPCRP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.4%; Score 85; DB 4; Best Local Similarity 30.3%; Pred. No. 0.18; Matches 37; Conservative 10; Mismatches
                                                                                                                                                                          13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
SEQ ID NO 30531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25561, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                              ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                   Best Local Similarity 27.9% Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             || |||:|
482 PRRRRRRMR 490
                                                                                                                                                                                                                                                                                                                                                                                                   112 PRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 PR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR 105
                                                                                     US-09-252-991A-25918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-252-991A-30531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-252-991A-30531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-252-991A-25561
SEQ ID NO 25918
LENGTH: 757
                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
```

```
APPLICAT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27628, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERQEINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 SRFMRKTARRKTPSTTANRPTPPS-----PTPTRASR------PRPRATRRKSRV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |::|| :: | :: || | :| | ASSRALLISALCACSAASTSMPATGAGARN-----SQAPMKPPANRLAPTTQAPASISNR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---SESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIRL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PTPSTPAIPTSSCRR-TVGIA----TAATSCSNPTKARTTRSASRVNISTDDSIPVSPT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 TPPGP-----STVFRPPTSS----RPLETPHCREIRIGIAGITITLSLCGC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 TPPWPTLREKSNSSGSTSASSVRRSPRASSRTRRACSSPRC-----TLSASICRC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 ANARAPTLRSATADNSEST-----GFKNVPDLRTDQP-KPPSKK------R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57;
                                                                                                                                                                                                                                                                                                                                                                                                  39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.2%; Score 83.5; DB 4; Length 384;
25.0%; Pred. No. 0.2;
.ive 21; Mismatches 36; Indels 57
                                                                                                                                                                                                                                                                                                                                   ch 13.2%; Score 83.5; DB 4; Length 133; 1 Similarity 27.5%; Pred. No. 0.048; 33; Conservative 12; Mismatches 36; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 PTSSRP-LETPHCREIRIGIAGITITLSLCGCAN-ARAPTLRSATADN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 SCDPSEYRV--SELKESLITTTPS-RPRIARR 117
PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR PLING DATE: 1998-02-18 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 25561 LENGTH: 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24427, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24427
                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 25.09
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-252-991A-27628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-252-991A-24427
```

```
Sequence 26926, Application US/09252991A

Patent No. 651795
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE
                                                                                                                                                                                                                                                                                                                                                         7 DTPPGPSTVFRPPTSSR-PLETPHCREIRIGIAGITITLSLCGCANARAPTLRSATADNS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 56334, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 DIPPGPSTVFRPPISSR-PLEIPHCREIRIGIAGITITLSLCGCANARAPTLRSATADNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SRSPSRRTSTNLNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 ESTGFKNVPD----LRTDQPKP-PSKKRSCDPSEYRVSELKESLITTTPSRPRTAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 ESTGFKNVPD----LRIDOPKP-PSKKRSCDPSEYRVSELKESLITITPSRPRTAR 116
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.8%; Score 81; DB 4; Length 195; 27.5%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.8%; Score 81; DB 4; Length 160; 26.7%; Pred. No. 0.12; ive 15; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                       38; Indels
                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                          ch 12.8%; Score 81; DB 1 Similarity 26.7%; Pred. No. 0.12 31; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 EKPOGKSP---SPTSSRSPSRSP----
                                                                                                                                                                                                                                                                                                                                                                                                                       9 EKPOGKSP---SPISSRSPSRSP
                                                                                                      , ORGANISM: Drosophila melanogaster US-09-270-767-41118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Conservative
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-26926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-270-767-56334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-270-767-56334
                                        LENGIH: 160
                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29784, Application US/09252991A
Patent, No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR |FILING DATE: 1998-02-18
PRIOR |FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 SLCGCANARAPTLRSATADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 PTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLR-----SATADNSESTGFKNV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 41118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 SRCRCTPSTTST-NTSSASRTSST----APAPRASRPTPSS-----PNPHRRSSRSTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 PTSIR-----CRSISVACRARSIICPMCWPTTRRPTRRTISCGSATGCIRQSRRCRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
12.9%; Score 81.5; DB 4; Length 135;
Best Local Similarity 27.8%; Pred. No. 0.083;
Matches 32; Conservative 12; Mismatches 42; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 PDLRIDQPKPPSKKRSCDPSEY-----RVSELKESLITITPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRRKTRPTGPTSDSRSRRPTAWPSRWPPTPRIS------PSSTVRSKRLK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 82.5; DB 4;
Pred. No. 0.12;
9; Mismatches 28;
PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILLING DATE: 1998-02-18
; PRIOR FILLING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILLING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27628
; LENGHH: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-270-767-41118
Sequence 41118
Sequence 41118
Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29784
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 33.3%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 ITTTPSRPRTAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 TSTTPSRPATTR 77
                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-27628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-29784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 29784
LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
```

This Page Biank (uspto)

```
December 23, 2004, 11:03:37; Search time 145 Seconds (without alignments) 299.677 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                      US-10-083-849B-1
632
1 MNALQEDTPPGPSTVFRPPT.......ESLITTTPSRPRTARRIRL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

1: \( \cgn2_6 \) ptodata/2 \) Pubpaa/NCT \\ PUBCOMB.pep:*

2: \( \cgn2_6 \) ptodata/2 \) Pubpaa/NCT \\ PUBCOMB.pep:*

2: \( \cgn2_6 \) ptodata/2 \) pubpaa/NCT \\ PUB \\ PUB.pep:*

4: \( \cgn2_6 \) ptodata/2 \) pubpaa/NCT \\ PUB \\ PUB.pep:*

5: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGO \\ PUB \\ PUB.pep:*

6: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGO \\ PUB \\ PUB.pep:*

7: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUB \\ PUB.pep:*

8: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

9: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

10: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

11: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

12: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

13: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

14: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

15: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

16: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

16: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

17: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

18: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

19: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

19: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

19: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

19: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*

19: \( \cgn2_6 \) ptodata/2 \) pubpaa/NGOB \\ PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1595201
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1595201 segs, 359116952 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                           Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STRUMBETES

					SUMMAKIES	
		dp				
Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
	632	100.0	121	14	US-10-083-849B-1	Sequence 1, Appli
7	629	99.5	121	14	US-10-083-849B-2	Sequence 2, Appli
m	627	99.2	121	14	US-10-083-849B-10	Sequence 10, Appl
4	627	99.3	121	14	US-10-083-849B-11	11,
Ŋ	627	99.5	121	14	US-10-083-849B-12	12,
ω	626	99.1	121	14	US-10-083-849B-14	14,
7	626	99.1	121	14	US-10-083-849B-15	15,
80	626	99.1	121	14	US-10-083-849B-16	16,
6	624	98.7	121	14	US-10-083-849B-13	13,
10	622	98.4	121	14	US-10-083-849B-17	17,
11	622	98.4	121	14	US-10-083-849B-18	
12	622	98.4	121	14	US-10-083-849B-19	Sequence 19, Appl
13	621	98.3	134	17	US-10-738-423-58	58

Sequence 60, Appl Sequence 1, Appli	Sequence 4, Appli	٠	Ñ	9	_		•						Sequence 120157,	Sequence 108424,	Sequence 162402,	Sequence 157638,	Sequence 7, Appli	Sequence 30, Appl	Sequence 143626,	Sequence 165015,				1492		1234				Sequence 66407, A
US-10-738-423-60 US-10-113-790-1	US-09-949-780-4	US-09-949-780-6	US-09-949-780-2		US-1			US-10-083-	US-1	US-1	US-10-437-	US-10-437-963-1	US-10-437-963-	US-10-437-	US-10	US-10-437-		US-10-312-352-		US-10	US-10		US-10	US-10-437-963-1	US-10		US-10	US-10-437-963	/ US-10-425-115-222583	S US-10-425-114-66407
	133 9														287 16					625 16				68 16						
														~	~	m	m	m	<u>ن</u>			<u>-</u>		268					~	m
98.3	97.5	97.5	97.5	96.2	96.0	96.0	95.5	95.6	95.3	94.6	16.3	14.8	14.2	13.5	13.4	13.1	13.1	13.1	13.1	13.1	13.0	13.0	12.9	12.9	12.9	12.8	12.8		12.7	12.7
621 621	616	616	616	809	607	607	909	604	602	598	103	93.5	90	85.5	84.5	83	83	83	83	82.5	82	82	81.5	81.5	81.5	81	81	81	80.5	80.5
14 15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	. 38	39	40	41	42	43	44	45

### ALIGNMENTS

```
FRATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1). [121)
OTHER INFORMATION: Apoptin (a small protein derived from chicken anemia virus) encc;
OTHER INFORMATION: ed by pCWV-Vp3 and by GFP-Apoptin constructs
US-10-083-849B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 632; DB 14; Length 121; ilarity 100.0%; Pred. No. 1.8e-55; Conservative 0; Mismatches 0; Indels 0;
            Sequence 1, Application US/10083849B
Publication No. US20030199009A1
GENERAL INFORMATION:
APPLICANT: No. US20030199009A1eborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Mumberg, Dominik
APPLICANT: Mumberg, Dominik
APPLICANT: Donner, Peter
TITLE OF INVENTION: Modifications of Apoptin
FILE REPRENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT PILING DATE: 2000-10-19
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 121;
JS-10-083-849B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TADNSESTGFKAVVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLIATTFSRPRTARRRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TADNSESTGFKNVPDLRIDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITATPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                               1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                            1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 121;
                                                                                                                                                                                                                                                                                 Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                              CCATION: (1)..(121)

THER INFORMATION: single point mutant T106A of Apoptin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)..(121)
OTHER INFORMATION: single point mutant T107A of Apoptin
                                                                                                                                                                                                                                                                            Query Match
99.2%; Score 627; DB 14;
Best Local Similarity 99.2%; Pred. No. 5.7e-55;
Matches 120; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 627; DB 14;
Pred. No. 5.7e-55;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/10083849B
Publication No. US20030199009A1
GENERAL INFORMATION:
APPLICANT: No. US20030199009A1eborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Donner, Peter
ITTLE OF INVENTION: Modifications of Apoptin
FILE REFERENCE: 2906-4966.1
CURRENT APPLICATION UNBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Version 3.1
SEQ ID NO 11
                                                                              TYPE: PRT ORGANISM: Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Chicken anemia virus
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 99.2%;
Best Local Similarity 99.2%;
Matches 120; Conservative
                                                                                                                                                       NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 1 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 Ľ 121
                                                                                                                                                                                                                             US-10-083-849B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-083-849B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-083-849B-11
                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Differs from Apoptin protein encoded by pCMV-Vp3 and by GFP-Apopt OTHER INFORMATION: in constructs by replacement of the arginine residue at position OTHER INFORMATION: 116 with a lysine residue
     61 TADNSESTGFKAVPDLRTDQPKPPSKKR$CDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TADNSESTGFKAVPDLRTDQPKRPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(121)
OTHER INFORMATION: Apoptin protein encoded by pIRESneo alanine mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.5%; Score 629; DB 14; Length 121; Best Local Similarity 99.2%; Pred. No. 3.6e-55; Matches 120; Conservative 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                          Sequence 2, Application US/10083849B;
Publication No. US20030199009A1;
GENERAL INFORMATION:
APPLICANT: No. US20030199009Aleborn, Mathieu APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Muhberg, Dominik
APPLICANT: Muhberg, Dominik
APPLICANT: Muhberg, Dominik
APPLICANT: Muhberg, Dominik
APPLICANT: Muhberg, 1006116, 11TLE, OF INVENTION: Medifications of Apoptin;
FILE REFERENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/10083849B
; Publication No. US20030199009A1
; GENERAL INFORMATION:
    APPLICANT: No. US20030199009Aleborn, Mathieu
    APPLICANT: Rohn, Jennifer Leigh
    APPLICANT: Mumberg, Dominik
    APPLICANT: Mumberg, Dominik
    TILE OF INVENTION: Modifications of Apoptin
    FILE REFERENCE: 2906-4996.1
    CURRENT APPLICATION NAMER: US/10/083,849B
    CURRENT FILING DATE: 2001-10-19
    PRIOR APPLICATION NUMBER: US 60/242,397
    PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MUTAGEN
                                                                           121 L 121
                                                                                                                          121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-083-849B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-083-849B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                       셤
                                                                           ઠે
                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

ö

9

```
TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                  61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLIETTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TADNSESTGFKNVPDLATTDQPKPPSKKRSCDPSEYRVSELKESLITETPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSBYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                 1 MWALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCAWARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                   1 MNALQEDTPPGFSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)..(121)
; OTHER INFORMATION: single point mutant T107E of Apoptin
US-10-083-849B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.1%; Score 626; DB 14;
99.2%; Pred. No. 7.2e-55;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/10083849B
; Publication No. US20030199009A1
GENERAL INFORMATION:
; APPLICANT: No. US20030199009A1eborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
; APPLICANT: Mumberg, Dominik
; APPLICANT: Mumberg, Dominik
; APPLICANT: Donner, Peter
; TILLE OF INVENTION: Modifications of Apoptin
; FILE REPERENCE: 2906-4996.1
; CURRENT APPLICATION NUMBER: US/10/083,849B
; CURRENT APPLICATION NUMBER: US 60/242,397
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/10083849B
; Publication No. US20030199009A1
; GENERAL INFORMATION:
APPLICANT: No. US20030199009Aleborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
; APPLICANT: Muhberg, Dominik
; APPLICANT: Domner, Peter
; TITLE OF INVENTION: Modifications of Apoptin
; FILE REFERENCE: 2906-4996.1
; CURRENT APPLICATION NUMBER: US/10/083,849B
; CURRENT PILING DATE: 2001-10-19
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.2
Matches 120; Conservative
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                           121 L 121
                                                                                                                                                                                                                                                                                                            121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-083-849B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-083-849B-16
                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                   ð
                                                                                              g
                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TADNSESTGFKNVPDLRIDQPKPPSKKRSCDPSEYRVSELKESLITTAPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNALOEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.1%; Score 626; DB 14; Length 121; 99.2%; Pred. No. 7.2e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 627; DB 14; Length 121;
Pred. No. 5.7e-55;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MUTAGEN
LOCATION: (1)..(121)
CHERION: NFORMATION: single point mutant T108A of Apoptin
US-10-083-9498-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) LOCATION: (1)..(121)
; OTHER INFORMATION: single point mutant T106E of Apoptin US-10-083-849B-14
                             Sequence 12, Application US/10083849B
Publication No. US20030199009A1
GENERAL INPORMATION:
APPLICANT: No. US20030199009A1
APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Mundberg, Dominik
APPLICANT: Wundberg, Dominik
APPLICANT: Wundberg, Dominik
APPLICANT: Wundberg, US/10/083,849B
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
FRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/10083849B
Publication No. US20030199009A1
GENERAL INFORMATION:
APPLICANT: No. US20030199009Aleborn, Mathieu
APPLICANT: Rohn, Jennifer Leigh
APPLICANT: Muhberg, Dominik
APPLICANT: Muhberg, Dominik
APPLICANT: Domner, Peter
ITLE OF INVENTION: Modifications of Apoptin
FILE REFERENCE: 2906-4996.1
FURNER FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/242,397
PRIOR PILING DATE: 2000-10-19
PRIOR PILING DATE: 2000-10-19
PRIOR PILING DATE: 2000-10-19
PRIOR FILING DASE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match . 99.24
Best Local Similarity 99.24
Matches 120, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 Ľ 121
                     -10-083-849B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 12
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 14
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
```

ઠે 셤 ઠ g ઠે 셤

```
61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            j LOCATION: (1)..(121)
; OTHER INFORMATION: double point mutation T106A107A of Apoptin
US-10-083-849B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)..(121); OTHER INFORMATION: double point mutant T107A108A of Apoptin US-10-083-849B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 98.4%; Score 622; DB 14;
Best Local Similarity 98.3%; Pred. No. 1.8e-54;
Matches 119; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.4%; Score 622; DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 119, Application US/10083849B
Sequence 119, Application US/10083849B
Publication No. US20030199009A1
GENERAL INFORMATION:
APPLICANT: No. US20030199009A1eborn, Mathieu
APPLICANT: Nohn, Jennifer Leigh
APPLICANT: Mumberg, Dominik
APPLICANT: Mumberg, Dominik
APPLICANT: Mumberg, Dominik
APPLICANT: Mumberg, Dominik
CURRENT : FILENG PATE: 2006-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT APPLICATION NUMBER: US 60/242,397
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
LENGTH: 121
                                                               Sequence 17, Application US/10083849B; Publication No. US20030199009A1; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: No. US20030199009A1eborn, Mathieu APPLICANT: Rohn, Jennifer Leigh APPLICANT: Donner, Peter TITLE REFERENCE: 2906-4996.1; TITLE REFERENCE: 2906-4996.1; CURRENT FILING DATE: 2001-10-19; PRIOR APPLICATION NUMBER: US/10/083,849B; CURRENT FILING DATE: 2001-10-19; PRIOR APPLICATION NUMBER: US 60/242,397; PRIOR FILING DATE: 2000-10-20; SOFTWARE: Patentin Version 3.1; ENGUID NO. 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i 121
                                                       US-10-083-849B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TADNSESTGFKAVVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTASRPRTARRRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTEPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                    Query Match 99.1%; Score 626; DB 14; Length 121; Best Local Similarity 99.2%; Pred. No. 7.2e-55; Matches 120; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.7%; Score 624; DB 14; Length 121; 99.2%; Pred. No. 1.1e-54; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                        ; LOCATION: (1)..(121)
; OTHER INFORMATION: single point mutant T108E of Apoptin US-10-083-849B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . LOCATION: (1) ...(121)
; OTHER INFORMATION: single point mutant P109A of Apoptin
US-10-083-849B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Publication No. US20030199009A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: No. US20030199009A1eborn, Mathieu APPLICANT: No. US20030199009A1eborn, Mathieu APPLICANT: Ponner, Peter ITLE OF INVENTION: Modifications of Apoptin FILE REFERENCE: 2906-4996.1
| CURRENT APPLICATION NUMBER: US/10/083,849B CURRENT FILING DATE: 2001-10-19
| PRIOR INLING DATE: 2000-10-20
| NUMBER OF SEQ ID NOS: 20
| NUMBER OF SEQ ID NOS: 20
| SEQ ID NO 13
| LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Chicken anemia virus
                                                                                                                                                      ORGANISM: Chicken anemia virus
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.2
Matches 120; Conservative
                                                                                                                                                                                                        NAME/KEY: MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-083-849B-13
                                                                                                                                   TYPE: PRT
                                                                                                                                                                                      FEATURE
```

ઠે g

셤 ò 셤

ò

Gaps

ö

Length 121;

셤

ò

à

```
61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 TADNSENTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRCIR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 MMALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Clairmont, C.
APPLICANT: Clairmont, C.
APPLICANT: Lin, S.
APPLICANT: Lin, S.
APPLICANT: Bellow. Confositions and merhods for Title OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES FILE REPRENCE: 8002-0599
CURRENT APPLICATION NUMBER: US/10/738,423
CURRENT FILING DATE: 2003-12-16
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 1999-10-04
PRIOR PLICATION NUMBER: 60/157,581
PRIOR PLICATION NUMBER: 60/157,637
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

98.3%; Score 621; DB 17; Length 140;
Best Local Similarity 98.3%; Pred. No. 2.7e-54;
Matches 119; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Score 621; DB 17;
Pred. No. 2.6e-54;
1; Mismatches 1;
     CURRENT FILING DATE: 2003-12-16

PRIOR APPLICATION NUMBER: US/09/645,415

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: G0/157,581

PRIOR PLING DATE: 1999-10-04

PRIOR PLING DATE: 1999-10-04

PRIOR PLING DATE: 1999-10-04

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PASLEEQ for Windows Version 3.0

SEQ ID NO S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 60 LENGTH: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 60, Application US/10738423
Publication No. US20040229338A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.3%;
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Bacteriophage US-10-738-423-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Bacteriophage US-10-738-423-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 L 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                               61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITAAPSRPRTARRIR 120
                                                                                                                                                                             61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TADNSESTGFKNVPDLATDQPKPPSKKRSCDPSEYRVSELKESLIATAPSRPRTARRIR 120
                                                                             1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                             1 MNALQEDTPPGFSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNALQEDIPPEPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-738-423-58

Sequence 58, Application US/10738423

Publication No. US20040229338A1

SEQUENCE APPLICANT: No. US20040229338A1

APPLICANT: King, I.

APPLICANT: Lin, S.

APPLICANT: Lin, S.

APPLICANT: Belcourt, M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES

FILE REFERENCE: 8002-059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.4%; Score 622; DB 14; Length 121; 98.3%; Pred. No. 1.8e-54; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MUTAGEN

COCATION: (121)

CTHER INFORMATION: double point mutant T106A108A of Apoptin
US-10-083-849B-19
98.3%; Pred. No. 1.8e-54;
tive 0, Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: No. US20330199009Aleborn, Mathieu APPLICANT: Rohn, Jennifer Leigh APPLICANT: Rohn, Jennifer Leigh APPLICANT: Mumberg, Dominik APPLICANT: Donner, Peter TITLE OF INVENTION: Modifications of Apoptin FILE REFRENCE: 2906-4996.1
CURRENT APPLICATION NUMBER: US/10/083,849B
CURRENT FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/10083849B
Publication No. US20030199009A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
Best Local Similarity 98.3
Matches 119, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.3
Matches 119; Conservative
                                                                                                                                                                                                                                                                                  121 L 121
                                                                                                                                                                                                                                                                                                                                  121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-083-849B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 19
                                                                                                                                                                                                                          a
a
                                                                             ઠે
                                                                                                                       a
                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

ઠ 셤 Š ઠે

```
Sequence 1, Application US/10113790
Sequence 1, Application US/10113790
Sequence 1, Application No. US20020176660A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: No. US20020176860A1eborn, Mathieu H.M.
APPLICANT: Zhang, Ying-Hui
APPLICANT: Zhang, Ying-Hui
APPLICANT: Zhang, Ying-Hui
APPLICANT: Trung OF 1005 No 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TADNSESTGFKOVVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TADNSESTGFKNVPDLRTDQAKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

98.3%; Score 621; DB 13; Length 523;
Best Local Similarity 98.3%; Pred. No. 1.3e-53;
Matches 119; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Apoptin-TK fusion protein US-10-113-790-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: December 23, 2004, 11:16:00 Job time: 146 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
121 1 121
                                                                                                     140 L 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 1 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
     ઠે
                                                                                         요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

٠,

```
5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2004
```

OM protein - protein search, using sw model

December 23, 2004, 10:52:36; Search time 39 Seconds (without alignments) 298.519 Million cell updates/sec Run on:

Title: Perfect score:

US-10-083-849B-1 632 1 MNALQEDTPPGPSTVFRPPT.......ESLITTTPSRPRTARRIRL 121 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed sed Minimum DB Maximum DB

Minimum Match O% Maximum Match 100% Listing first 45 summaries Post-processing:

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
1: pir3:\*
: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	629	99.5		~	B39926	hypothetical prote
71	919	97.5		~	B48343	_
٣	84	13.3	247	~	T32514	hypothetical prote
4	83	13.1	377	~	A48018	
2	81.5	12.9		0	T13653	hypothetical prote
9	80.5	12.7	748	~	D84595	pEARLI 4 protein [
7	80.5	12.7	3570	~	T45025	mucin MUCSB, trach
æ	80	12.7	1388	N	A53317	collagen alpha 1(X
6	79.5	12.6		~	S28394	probable serine/th
10	79.5	12.6		~	T15269	hypothetical prote
11	78.5	12.4		~	D70752	probable lprE prot
12	78.5	12.4	475	0	D86209	protein F22G5.18 (
13	78.5	12.4		~	T29324	hypothetical prote
14	78	12.3	278	7	T46458	
15	2	12.2		N	S38148	
16		12.1		N	T30760	hypothetical prote
17	76.5	12.1		~	847539	ų
18	76.5	12.1		~	T19893	hypothetical prote
19	76.5	12.1		~	T09219	н
20	75.5	11.9		N	S47091	cyclase-associated
21	75.5			~	C43674	US4 protein - huma
22	75	11.9	9	~	T17221	hypothetical prote.
23	74.5	11.8	e	~	A41558	
24	74	11.7	4	ч	S24354	p53-binding protei
25	73.5	11.6		П	A47547	serine proteinease
26	73	•		~	862349	L71-3 protein - fr
27	73	11.6	493	N	S36488	E2 protein - human
28	73	11.6	631	0	A54659	•~
29	72.5	11.5	416	~	S27198	ы

mucin 2 precursor,	hypothetical prote	hypothetical prote	DNA (cytosine-5-)-	E2 protein - human	hypothetical prote	nascent polypeptid	homeotic protein H	glycoprotein G - B	hypothetical prote	hypothetical prote	hypothetical prote	35K proline-rich p	hypothetical prote	104K microneme-rho	KIAA0013 protein (	
A43932	S40766	T22845	JE0378	W2WL47	T29776	T30826	S34164	849525	T48107	T25592	T34513	A56561	T36204	A44945	A59431	
7	~	~	~	-	~	~	7	~	7	7	~	7	7	~	7	
3020	1232	1250	1622	206	1046	2187	411	593	975	1624	3507	315	407	924	1023	
11.5	11.4	11.4	11.4	11.3	11.3	11.3	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2	
72.5	72	72	72	71.5	71.5	71.5	7.1	71	71	71	71	70.5	70.5	70.5	70.5	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

RESULT 1

```
hypothetical protein 2 - chicken anemia virus
CiSpecies: chicken anemia virus, CAV
CiSpecies: chicken anemia virus, CAV
CiSpecies: chicken anemia virus, CAV
CiSpate: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 09-Jul-2004
CiAccession: B3926
RiNoteborn, M.H.M.; de Boer, G.F.; van Roozelaar, D.J.; Karreman, C.; Kranenburg, O.; V.
Virol. 65, 3113-3139, 1991
A; Title: Characterization of cloned chicken anemia virus DNA that contains all elements
A; Reference number: A39926, MUID:91237831; PMID:1851873
A; Accession: B3928
A; Residuate type: DNA
A; Residuate type: DNA
A; Residuates: 1-12 cNOT>
A; Residuates: 1-12 cNOT>
A; Crosss-references: UNIPROT: Q99152; GB:M55918; NID:9323250; PIDN:AAA91823.1; PID:932325
C; Comment: This virus is unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MNALQEDTPPGESTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 629; DB 2; Length 121;
Pred. No. 2.1e-52;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 99.2
Matches 120, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
B39926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

# B48343

hypothetical 13K protein - chicken anemia virus (isolate Cux-1)
C;Species: chicken anemia virus, CAV
C;Species: chicken anemia virus, CAV
C;Date: 17-Feb-1994 #sequence\_revision 16-Apr-1999 #text\_change 09-Jul-2004
C;Accession: B48343
R;Meehan, B.M.; Todd, D.; Creelan, J.L.; Earle, J.A.; Hoey, E.M.; McNulty, M.S.
A;Title: Characterization of viral DNAs from cells infected with chicken anaemia agent: A;Reference number: A48343; MUID:92296898; PMID:1605740

A,Accession: B48343 A;Molecule type: DNA A;Residues: 1-121 cMEE> A;Residues: 1-121 cMEE> A;Cross-references: UNIPROT:Q99152; GB:M81223; NID:g323254; PIDN:AAA42883.1; PID:g32325 A;Note: the authors translated the codon ACA for residue 41 as Gly A;Note: sequence extracted from NCBI backbone (NCBIN:106168, NCBIP:106170)

Query Match

97.5%; Score 616; DB 2; Length 121;

```
Query Match
Best Local Similarity 26.9%
Matches 32, Conservative
                                                                                                                                                                                                                                                        A; Gene: GDB: MUC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S:
Matches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
D84595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mucin 7 precursor, salivary - human

N;Alternate names: mucin, MG2; mucin, MG2a-T1; mucin, MG2a-T2; mucin, MG2b-T2
C;Species: Home saplens (man)
C;Date: 16-Feb-1994 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48018; S29115; S29116; S29114
C;Accession: A48018; S29115; S29116; S29114
J. Biol. Chem. 268, 20563-20569, 1993
A;Title: MOlecular cloning, sequence, and specificity of expression of the gene encoding A;Reference number: A48018; MUID:93388636; PMID:7690757
A;Accession: A48018
A;Molecule type: mRNA
A;References: UNIPROT:Q9UCD8; GB:L13283
A;Reperimental source: submandibular gland
A;Note: sequence extracted from NCBI backbone (NCBIN:137719, NCBIP:137720)
A;Rosel-mental source: submandibular gland
A;Note: sequence extracted from NCBI backbone (NCBIN:137719, NCBIP:137720)
A;Reperimental sectuated from NCBI backbone (NCBIN:137719, NCBIP:137720)
A;Reference number: S29114; MUID:93075006; PMID:1445223
A;Title: Structural features of the low-molecular-mass human salivary mucin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-274 <TIN>
A;Cross-references: UNIPROT:O44145; EMBL:AF036692; PIDN:AAB88324.1; GSFDB:GN00022; CESP:A;Experimental source: strain Bristol N2; clone C44B12
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                   61 TADNSESTGSKNVPDLATDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRCIR 120
                                                                                                                                                                                                     61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 NNQQYDAPAYGPSFIQRP----RPFERQACRN-----TAIYSQESCQNCCSISSRAA 156
                                                                                                                                               1 MWALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCAWARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TADNSESTGFKNVPDLRTD----QPKPPSKK----RSCDPSEYRVSELKESLITTTP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Caenorhabditis elegans
Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004;
Accession: T32514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 NALQEDTPP-GPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                 1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Gaps
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: CESP:C44B12.1
A,Map position: 4
A;Introns: 28/3, 82/1, 164/1; 192/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C44B12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 247;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RiTin-Wollam, A. submitted to the EMBL Data Library, December 1997 A; Description: The Equence of C. elegans cosmid C44B12. A; Reference number: 221183
. 3.5e-51;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C44B12.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
13.3%; Score 84; DB 2;
Best Local Similarity 29.7%; Pred. No. 1.2;
Matches 35; Conservative 13; Mismatches 46
                  98.3%; Pred. No. 3.5e-
ive 0; Mismatches
                                           ;
0
                                              119; Conservative
                Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: T32514
                                                                                                                                                                                                                                                                                                            121 L 121
                                                                                                                                                                                                                                                                                                                                                               121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S29115
                                                                                                                                                                                                                                                셤
                                                                                                 ઠે
                                                                                                                                               셤
                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
```

```
A;Accession: 52916
A;Molecule type: protein
A;Residues: 'S',71-79',N',81-86,'XX',89,'X',91,'P' <RE2>
A;Accession: S29114
A;Molecule type: protein
A;Residues: 143-145,'X',147,'XXX',151-152,'X',154-158,'X',160-161,'A',163-164,'XX',167-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pEARLI 4 protein [imported] - Arabidopsis thaliana ($\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\circ{\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aypothetical protein 95B7.2 - fruit fly (Drosophila melanogaster)
C.Species: Drosophila melanogaster
C.Species: Drosophila melanogaster
C.Species: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C.Accession: T13653
R.Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
Submitted to the EMBL Data Library, April 1999
A.Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A.Reference number: Z17694
A.Accession: T13653
A.Accession: T13653
A.Accession: T13633
A.Accession: T1982
A.BER, A.BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:138799; OMIM:158375
A;Map position: 4q13-4q21
C;Keywords: glycoprotein
F;1-18/Domain: signal sequence #status predicted <SIG>F;1-18/Domain: signal sequence #status predicted <MAT>F;19-377/Product: mucin 7, salivary #status predicted <MAT>F;97,128,135,146,312/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 PTPPATTPAPPSSSAPPETTAAPPTPSATTPAPLSSSAPPETTÄVPPTPSATTLÜPSSA- 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 RSATADNSEST--GFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 GSVTWHNCPGTRASARVIQKOMKQDQTRPMTP----PPSEREPNKKEEKAAQKTPSQLKT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEELSKOPPPPLTOPPPSSSVSIEEP----LPNGKGGGAVVVN----SIAKLPEEELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 PPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSATADNSEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAP---TL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 GPKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 13.1%; Score 83; DB 2; Length 377; Local Similarity 29.2%; Pred. No. 2.3; length 377; les 31; Conservative 8; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 ---SAPPETTAAPPTPSATTPAPPSSPAPQETTAAPITTPNSSPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.9%; Score 81.5; DB 2; 26.9%; Pred. No. 9.1; tive 20; Mismatches 50;
```

Thu

```
A; Status: preliminary
                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S28778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Genetics:
A,Gene: GDB:COL15A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S28394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S46821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45025
R;Destion: Lu; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A.
J. Biol. Chem. 272, 3168-3178, 1997
A;Title: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alternat A;Reference number: Z22899; MUID:97166151; PMID:9013550
A;Accession: T45025
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                             A;Status: preliminary
A;Astatus: preliminary
A;Residus: 1-748 «STO»
A;Cross-references: UNIPROT:Q9SKR5; GB:AE002093; NID:g4803947; PIDN:AAD29820.1; GSPDB:GN
A;Gene: At2g20960
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53317; A35146; S28778
R;Kivlrikko, S.; Heinaemaeki, P.; Rehn, M.; Honkanen, N.; Myers, J.C.; Pihlajaniemi, T.
J. Biol. Chem. 269, 4773-4779, 1994
A;Title: Primary structure of the alphal chain of human type XV collagen and exon-intron A;Reference number: A53317; MuID:94148920; PMID:8106446
A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A,Reference number: A84420; MUID:20083487; PMID:10617197
A,Accession: D84595
                                                                                                                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2089 TPPVPNTTATTHGRSLPPSSPH----TVPTAWTSATSGILGTTHITEP-----S 2133
                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reaidues: 1-3570 <DES>
A; Cross-references: EMBL: 272496; NID:91834502; PIDN:CAA96577.1; PID:91834503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLIT-----TTPSRPRTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 TPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSATADNSES
                                                                                                                                                                                                                                                                                                                                                                       7 DTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSATADN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2134 TGTSHTPAATTGTTQPSTPALSSPHPSSRTTESPPSPGTTTPGHTRGTSR 2183
                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 TGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARR 117
                                                                                                                                                                                                                                                                  Score 80.5; DB 2; Length 748; Pred. No. 8.4; 9; Mismatches 47; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 3570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mucin MUC5B, tracheobronchial [imported] - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 80.5; DE; Pred. No. 46; 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collagen alpha 1(XV) chain precursor - human N;Alternate names: procollagen alpha 1(XV) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.7%;
26.4%;
                                                                                                                                                                                                                                                                    12.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 26.4*
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 RRRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORRGR 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: MUCSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
```

```
A;Residues: 1-1388 <KIV>
A;Residues: 1-1388 <KIV>
A;Residues: 1-1388 <KIV>
A;Residues: 1-1388 <KIV>
A;Cross=references: UNTROT:P39059; GB:L25280
A;Note: nucleotide sequence and conceptual translation not complete
R;Muragaki, Y:, Abe, N.; Ninomiya, Y:; Olsen, B.R.; Ooshima, A.
J. Biol. Chem. 269, 4042-4046, 1994
A;Title: The human alpha1(XV) collagen chain contains a large amino-terminal non-triple
A;Reference number: A53146; MUID:94140817; PMID:8307960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-9,'S',11-48,'V',50-94,'A', 96-149,'A',151-203,'V',205-408,'A',410-569 cMUR
A; Cross-references: GB:D21230; NID:9415605; PIDN:BAA04762.1; PID:041005294; PID:9460703
R; Myers, J.C.; Kivirikko, S.; Gordon, M.K.; Dion, A.S.; Pihlajaniemi, T.
Proc. Netl. Acad. Sci. US.A. 89; 10144-10148, 1992
A; Title: Identification of a previously unknown human collagen chain, alphal(XV), charach, A; Reference number: S28778; MUID:93066196; PMID:1279671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable serine/threonine-specific protein kinase (EC 2.7.1.-) STE20 - yeast (Saccharom VALebrate names: protein YHL007c (Species Saccharomyces cerevisiase (Species Saccharomyces cerevisiase (Species 17-Apr-1993 #text_change 16-Aug-2004 (SAccession: S28394; S46821; Ā47324; A57493 #text_change 16-Aug-2004 (Sieberer, B.; Dignard, D.; Harcus, D.; Thomas, D.Y.; Whiteway, M. BMBO J. 11, 4815-4824, 192 A;Title: The protein kinase homologue Ste20p is required to link the yeast pheromone re A;Reference number: S28394; MUID:93099855; PMID:1464311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-939 <LEB>
A;Cross-references: UNIPROT:Q03497; EMBL:M94719; NID:g172746; PIDN:AAA35111.1; PID:g172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A,Residues: 1-939 c.RAV.
A,Gross-references: BMBL:U11581; NID:9508676; PIDN:AAB69747.1; PID:9508679; MIPS:YHL007.
R;Ramer, S.W.; Davis, R.W.
R;Ramer, S.W.; Davis, R.W.
A;Ramer, S.W.; Davis, R.W.
A;Title: A dominant truncation allele identifies a gene, STE20, that encodes a putative
A;Reference number: A47324; MUID:93133807; PMID:8421676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 TEPGSHVSQEAPAFSVPVMTHRWNRFAMIVQGEEVTL-LVNCEEHSKIPFQRSSQALAFE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 TPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGC-ANARAPTLRSATA---- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DNSESTG---FKNVPDLRTDQPKPPSKKRSCDPSBYR------VSE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 9q21-9q22
F;1-22/Domain: signal sequence #status predicted <SIG>
F;1-23/Domain: signal sequence | Status predicted <MAT>
F;23-1388/Product: collagen alpha 1(XV) chain #status predicted <MAT>
F;1216-1388/Region: multiplexin collagen carboxyl-terminal homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.7%; Score 80; DB 2; Length 1388 Best Local Similarity 25.5%; Pred. No. 18; Matches 35; Conservative 18; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RiFavello, T.

Submitted to the EMBL Data Library, June 1994
A; Description: The sequence of S. cerevisiae cosmid L5018.
A; Reference number: 346798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 544-640,'P',642-811,'P',813-1252 <MYE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GDB:132578; OMIM:120325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 LKESLITTTPSRPRTAR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 ILEA-VTYTQASPKEAK 273
```

```
Cispecies: Mycobacterium tuberculosis
Cipate: 17-ul-1998 #eequence_revision 17-Jul-1998 #text_change 09-Jul-2004
Riconaria: Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamilin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature: 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70752
A;Accession: D70752
A;Residues: 1-202 <COL>
A;Residues: 1-202 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RyTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., Matere, O.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Actuals preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9LNW7; GB:AE005172; NID:g8778565; PIDN:AAF79573.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q11065, GB:Z77137; GB:AL123456; NID:g3261593; PIDN:CAB00900 A;Experimental source: strain H37Rv C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -ESLITTIPSRP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 ----PSLSTAHPAPPSSEPSPPSATAAPPSNHSAAPVDPCAVNLASPTIAKVVSELPRDP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 pg---vwsppcpttp------kvgvvaalvaattrgcgsg-----bstvaktprat- 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein F22G5.18 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 PGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSATADNSESTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 202;
                                                                                                                                                                                                               probable lprE protein - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 FKNVPDLRTDQPKPPSKKRS-----CDPSEYRVSELK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 78.5; DB 2;
Pred. No. 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 78.5; DE; Pred. No. 3.1; 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.4%; 23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.4%;
23.0%;
            ---RRR 118
                                                                  652 ŘÍSTVVPMITŘŘŘ 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 23.0%
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-475 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 RT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 RS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: F22G5.18
A,Map position: 1
            113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Gene: 1prE
                                                                                                                                                         RESULT 11
                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
A; Molecule type: DNA
A; Residues: 1-18, 'S', 20-133, 'M', 135-270, 'S', 272-939 <RAM>
A; Cross-references: EMBL:L04655; NID:g172586; PIDN:AA435038.1; PID:g172586
A; Note: sequence extracted from NCBI backbone (NCBIN:122769, NCBIP:122774)
R; Wu, C.; Whiteway, M.; Thomas, D.Y.; Leberer, E.
Biol. 'Chem. '270 issaye15995, 1995
A; Title: Molecular characterization of Ste20p, a potential mitogen-activated protein or
A; Reference number: A57493; MUID:95332294; PMID:7608157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: protein kinase homology. C;Superfamily: protein kinase; signal tr. C;Rywonds. ATP; phosphotransferase; serine/threonine-specific protein kinase; signal tr. F;618-871/Domain: protein kinase homology «KIN» P;626-634/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :Cross-references: EMBL:AF003386; NID:g2088833; PID:g2088836; PIDN:AAB54252.1; GSPDB:GN
Brperimental source: strain Bristol N2; clone F59B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description: signal transduction; required for pheromone signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                542 PASPKA'ISHPSTPAKSPQKTPQKKKEITPVEVKIEEIKEEEDVTPSQSPPATQTPRSRGR 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIHSSASKKTEKPETPRAESPD---PLPPPPSKKRPKEPSQ-----EPSTNTSSKRP 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Caenorhabditis elegans
Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
Accession: T15269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 QEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSATADN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 QVSTPPANSFNKFPPSTS----DSHNYGSRTGTPMSNHVMS-----PTLNT---DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SESTGFKNVPDLRTDQPKPPSKKRSCDP----SEYRVSELKESLITTTPSRPRTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPGPSTVFRPPTSSR-PLETPHCR-----EIRI----GIAGITITLSLCGCANARA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTLRSATADNSE--STGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 1082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 2
A;Introns: 122/2; 193/2; 254/3; 306/3; 459/2; 819/3; 859/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RiJohnson, D. Bull. Data Library, May 1997 submitted to the EMBL Data Library, May 1997 A;Description: The sequence of C. elegans cosmid F59E12. A;Reference number: Z18318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lypothetical protein F59E12.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status! preliminary; translated from GB/EMBL/DDBJ
:Molecule type: DNA
:Residues: 1-1082 <JOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
12.6%; Score 79.5; DB
Best Local Similarity 30.1%; Pred. No. 13;
Matches 37; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.6%; Score 79.5; DE
27.1%; Pred. No. 16;
:ive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: SGD:S0000999; MIPS:YHL007c;Map position: 8L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Watch
Best Local Similarity 27.1%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 757-784 <WUA>
                                                                                                                                                                                                                                                                     Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CESP: F59E12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 RRI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSI 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminar
                                                                                                                                                                                                                                             Accession: A57493
                                                                                                                                                                                                                                                                                                                                                                                       A, Gene: SGD:STE20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55
                                                                                                                                                                                                                                                                                                                                                            Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
EMBL: Z28296; NID: 9486542; PID: 9486543; GSPDB: GN0001
  58 PGPSRQSAPRARARGP--TPRTEEAAWAAMALTFLLVLLTLATLCTRLHRNFRRGESIYWG 115
                                                                                                C,Species: Saccharomyces cerevisiae
C,Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 SGSKLPTFKKASSSTSNLPSFKKADHSRQPIVKETDSFKPPSFKMTTEPKVYRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 ANARAPTLRSATADNSESTGFKNVPDLR-----TDQPKPPSKKRSCDPSEYRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                       hypothetical protein YKR071c - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Indels
                                                                                                                                                                                                                                                                                                                                                                                          R;Pohl, T.M.; Pohl, F.M.
submitted to the Protein Sequence Database, March 1994
A;Reference number: S37897
                                                                60 ATADNSESTGFKNVPDLRTDQPKPPSKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 77; DB
Pred. No. 7.9;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: December 23, 2004, 11:04:16 Job time : 41 Becs
                                                                                                                                                      96 RVSELKESLITTTPSRPRTARR 118
                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-348 <POH>
A;Cross-references: UNIPROT:P36152;
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Genetics:
A,Gene: SGD:DRE2; MIPS:YKR071c
A,Cross-references: SGD:S0001779
A,Map position: 11R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 33.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S38148
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S38148
                                                                                                                                                                                                                                                               RESULT 15
                                                                                                  g
                                                                                                                                                 ò
                                                                                                                                                                                     g
                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P91400; EMBL:U80450; PIDN:AAB37830.1; GSPDB:GN00019; CESP:Md
A;Experimental source: strain Bristol N2; clone M01E11
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                          :: |: || || || SAQKPTPGGPLTHDLNVPYEGTEEYETPTAEMLFPPT---PLQTP------- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PTMQSTASRISTLTA 105
                                            -----VFRPPTSSRPLETPHCREIRIGIAGITI 42
                                                                                                                               ----- PSKKRS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 PGPSTVPRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSATADNSESTG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 PGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRS------ 59
                                                                                                                                                                                                                                                                                                                                                                    pothetical protein M01E11.6 - Caenorhabditis elegans
Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein DKFZp434M102.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: T46458
R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23028
A;Accession: T46458
    65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 278;
  38; Indels
                                                                                                                             43 TLSLCGCANARAPTLRSATADNSESTGFKNVPDLRTDQPKP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 FKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Pauley, A.; Gattung, S.
submitted to the EMBi Data Library, November 1996
A;Description: The sequence of C. elegans cosmid MO1E11.
A;Reference number: 220605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:09NTBS; EMBL;AL137404
A;Experimental source: adult testis; clone DKFZp434M102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: T29324
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DB
A;Residues: 1-587 <PAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.3%; Score 78; DB 2
23.8%; Pred. No. 5;
tive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.4%; Score 78.5; DE
Best Local Similarity 23.3%; Pred. No. 10;
Matches 24; Conservative 12; Mismatches
  Mismatches
                                                                                                                                                                                                                  90 CDPSEY--RVSELKESLITTTPSRPRTARR 117
                                                                                                                                                                                                                                             A;Introns: 52/1; 314/3; 460/1
C;Superfamily: kinesin motor domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 PERSAMAKPASCSRPI------
  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 23.8*
Matches 34; Conservative
  Conservative
                                          2 NALQEDTPPGPST--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Residues: 1-278 <AAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Note: DKFZp434M102.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CESP: M01E11.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: T29324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Map position: 1
35;
                                                                                                                                                                     104
  Matches
                                                                                                                                                                   셤
                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                      g
                                                                                셤
                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
```

ή;

		*
	e 1	
 	-· ··· - · - · - · - · · · · · · · ·	
	*	•

Ŀ

```
091n93 chicken ane 091n97 chicken ane 091n97 chicken ane 091na2 chicken ane 091na8 chicken ane 091nb1 chicken ane 091nb7 chicken ane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Chowdhury S.M.Z.H., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Pathogenicity, sequence and phylogenetic analysis of Malaysian Chicken anaemia virus obtained after low and high passages in MSB-1 cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=14648297;
Chowdhury S.M., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
Md-Zain B.M., Kono Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 632; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 7e-52;
Matches 121; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhong L.K., Cheng H.Q., Yun L.L.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases
EMBL, AR190102; AAM73651.1;
GO, GO:0042025; C:host cell nucleus; IEA.
GO; GO:0019051; P:induction of apoptosis by virus; IEA.
InterPro; IPR006858; CAV VP3.
ERMI, PR04711; CAV VP3.
ERMEDAN, PR04711; CAV VP3.
ERMEDAN, PR04711; CAV VP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kono Y.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses, ssDNA viruses; Circoviridae; Gyrovirus
NCBI_TaxID=12618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AA
                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
Q91N90
Q91N93
Q91N93
Q91NA2
Q91NAA
Q91NB1
Q91NB1
Q91NB7
Q91NB7
Q91NB7
Q91NB7
Q91NB7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arch. Virol. 148:2437-2448(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 05-JUL-2004 (TrEMBLrel. 27,
                                                     00000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
     Chicken anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
     444444666

4444444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666

444666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VP3 (Apoptin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 L 121
  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=vp3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8JJJJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
     요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     099152 chicken ane 090wx2 chicken ane 090wx2 chicken ane 090wx3 chicken ane 090wx3 chicken ane 090wx3 chicken ane 090wy3 chicken ane 090wy3 chicken ane 091x0 chicken ane 091x0 chicken ane 090wx1 chicken ane 091x0 chicken ane 081x1 chicken ane 085x1 chicken ane 065x1 chicken ane
                                                                                                                                                                                           (without alignments)
358.868 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                 US-10-083-849B-1
632
1 MNALQEDTPPGPSTVFRPPT......BSLITTTPSRPRTARRIRL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                    December 23, 2004, 10:37:16 ; Search time 194 Seconds
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                        1825181 segs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  091NAS
VP3 CAV82
09J1K0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8JQ32
VP3_CAV26
Q6R<u>5</u>33
AAR97919
Q6GVG8
                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBJUU2
VP3 CAVC1
Q9DWX2
O41448
VP3 CAVCI
Q9DHB0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9DWX3
Q91N81
Q8JNK4
Q75ZF9
Q9WB33
Q9DWW8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q91HB6
Q91ZU6
Q9DWW9
                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 039313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OBJPT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            096671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9DWX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9IEZ4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9MMG60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9DWX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              988.7.7.998.7.7.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.998.3.99
                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  608
605
596.5
580
580
494
                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
```

01-OCT-1996 (01-OCT-1996 (28-FEB-2003 (

CAVC1

RESULT 2

```
61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TADNSESTGFKNVPDLRTDOPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNALQDDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                     Scott A.N.J., McNulty M.S., Todd D.,
"Characterisation of a chicken anaemia virus variant population that
resists neutralisation with a group-specific monoclonal antibody.";
Arch. Virol. 146:713-728 (2001).
BMBL, AJ297682; CAC14788.1; -.
GO; GO:0042025; Chost cell nucleus; IEA.
GO; GO:00551; Psinduction of apoptosis by virus; IEA.
PinterPro; IPR006858 CAV VP3.
Pfam: PF04771; CAV VP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3]
SEQUENCE FROM N.A.
MEDLINE=98001356; PubMed=9343191;
MEDLINE=98001356; PubMed=9343191;
Mechan B.M., Todd D., Creelan J.L., Connor T.J., McNulty M.S.;
"Investigation of the attenuation exhibited by a molecularly cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of viral DNAs from cells infected with chicken anaemia agent: sequence analysis of the cloned replicative form and transfection capabilities of cloned genome fragments."; Arch. Virol. 124:301-319(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning of an attenuated chicken anaemia virus isolate following repeated cell culture passage.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Todd D., Connor T.J., Calvert V., Creelan J.L., Meehan B.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-92296898; PubMed=1605740;
Mechan B.M., Todd D., Creelan J.L., Earle J.A.P., Hoey B.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 629; DB 2; Length 14.1
Pred. No. 1.3e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF04771, CAV VP3, T. SEQUENCE 121 AA; 13284 MW, 82ABB3865CCBACES CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                041448 PRELIMINARY; FKI; LATER O41448; 01-JAN-1998 (TrEMELrel. 05, Created) 01-JAN-1998 (TrEMELrel. 05, Last sequence update) 05-JUL-21094 (TrEMELrel. 27, Last annotation update) Orf3; 13 kDa protein (VP3).
                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                         Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
NCBI_TaxID=12618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.2%; Pred. No. 1...
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            following repeated cell culture passage.";
Avian Pathol. 24:171-187(1995).
                                              Created)
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=21296594; PubMed=11402858;
                                       (TrEMBLrel. 16, C
(TrEMBLrel. 16, I
(TrEMBLrel. 24, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.2
Matches 120, Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=12618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 L 121
                                       01-MAR-2001
01-MAR-2001
01-JUN-2003
                                                                                                             VP3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McNulty M.S
                                                                                                                                       Name=VP3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TADNSESTGFKAVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTAKRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                  [1] —
SEQUENCE FROM N.A.
MEDLINE-91237831; PubMed=1851873;
MEDLINE-91237831; PubMed=1851873;
Noteborn M.H.M., de Boer G.F., van Roozelaar D.J., Karreman C.,
Kranenburg O., Vos J.G., Jeurissen S.H.M., Hoeben R.C., Zantema A.,
Koch G., van Ormondt H., van der Eb A.J.;
"Characterization of cloned chicken anemia virus DNA that contains all
elements for the infectious replication cycle.";
J. Virol. 65:3131-3139(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of viral DNAs from cells infected with chicken anaemia agent: sequence analysis of the cloned replicative form and transfection capabilities of cloned genome fragments.";
Arch. Virol. 124:301-319(1992)

-I-FUNCTION: May act as transcriptional regulator. Induces apoptosis in infected cells. Element of infectious replication cycle.
-I- SUBCELLULAR LOCATION: Nuclear; nucleus of infected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNALOEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNALQEDIPPGPSTVPRPPISSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92296898; PubMed=1605740;
Meehan B.M., Todd D., Creelan J.L., Earle J.A.P., Hoey E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.5%; Score 629; DB 1; Length 121; 99.2%; Pred. No. 1.3e-51; tive 1; Mismatches 0; Indels
                                                                                                                                                                Apoptin (VP3).

Chicken anemia virus (German isolate Cuxhaven-1) (CAV).

Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 70 F -> S (in Ref. 2).
116 K -> R (in Ref. 2).
118 118 R -> C (in Ref. 2).
121 AA, 13270 WW, D2AAB3869BC12A3E CRC64,
                                                                                                      (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
```

InterPro; IPR006858; CAV VP3. Pfam; PF04771; CAV VP3; 1. Apoptosis; Nuclear protein.

120; Conservative

Matches

L 121 L 121

121 121

RESULT 3 | Q9DWX2

61

셤 8 요 ò

ठ

Local Similarity

SEQUENCE Query Match

CONFLICT

EMBL; M55918; AAA91823.1; -. EMBL; M81223; AAA42883.1; -.

SEQUENCE FROM N.A.

PIR; B39926; B39926. PIR; B48343; B48343

٤,

ð 셤 ò 셤 ઠે 셤

```
Pred. No. 4e-51;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=21296594; Pubmed=11402858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 16, C
(TrEMBLrel. 16, I
(TrEMBLrel. 24, I
                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 16, C
(TrEMBLrel. 16, I
(TrEMBLrel. 27, I
99.2%;
 Best Local Similarity 99.2
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                         121 L 121
                                                                                                                                                                                                                                             L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001
01-MAR-2001
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                 VP3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VP3 protein.
                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=VP3;
                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=VP3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9DWX3;
                                                                                                                                                                                                                                                                                                                                                            Q9DH80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9DWX3
                                                                                                                                                                                                                                                                                                                                        Q9DH80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
                                                                                                                                                                                                                                                                                                   RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9DH80
                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    유
                                                                                            셤
                                                                                                                               ò
                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                  61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                     TADNSESTGFKAVVPDLRTDOPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                               MNALQEDTPPGEPSTVFRPPTSSRPLETPHCREIRIGIAAITITLSLCGCANARAPTLRSA 60
chicken anemia virus isolate by utilizing a chimeric virus approach.";
J. Virol, 71:8362-8367(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Renshaw R.W.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May act as transcriptional regulator. Induces apoptosis
in infected cells. Element of infectious replication cycle.
-!- SUBCELLUIAR LOCATION: Nuclear; nucleus of infected cells.
                                                                                                                                                                                                                                                                                                                                        1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97126092; PubMed=8971016; Renshaw R.W., Soine C., Weinkle T., O'Connell P.H., Ohashi K., Watson S., Lucio B., Harrington S., Schat K.A.; Ahypervariable region in VPl of chicken infectious anemia virus mediates rate of spread and cell tropism in tissue culture."; J. Virol. 70:8872-8878(1996).
                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                             99.1%; Score 626; DB 2; Length 121; 99.2%; Pred. No. 2.6e-51; Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.7%; Score 624; DB 1; Length 121;
                                                                                          to the EMBL/GenBank/DDBJ databases.
                                                                       McKenna G.F.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; U66304; AAC58477.1; ---
EMBL; AJ336295; CAD60259.1; ---
GO; GO:0019051; P:induction of apoptosis by virus; IEA.
GO; GO:0019051; P:induction of apoptosis by virus; IEA.
InterPro; IPR006888; CAV VP3.
Pfam; PF04771; CAV_VP3; I.
SEQUENCE 121 AA; 13312 MW; E4AAB75960F2C5C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13245 MW; D2AAB39C2BD61A3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptin (VP3).
Chicken anemia virus (USA isolate CIA-1) (CAV).
Viruses, sebna virus (ircoviridae; Gyrovirus.
VCBI_TaxID=73478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR006858; CAV VP3.
Pfam; PF04771; CAV VP3; T.
Apoptosis; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L14767; AAD09423.1; -
                                                                                                                                                                                                                                                                                  Best Local Similarity 99.2
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISION TO 50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VP3_CAVCI
P54094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VP3_CAVCI
```

```
ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TADNSESTGFKNVPDLATTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                              61 TADNSESTGFKAVVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                61 TADNSESTGFKNVPDLKTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRCIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNALQEDTPPGPSTVFRPATSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                              1 MNALQEDTPPGESTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                        1 MNALQEDIPPGPSTVFRPPISSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNALQEDIPPGESTVFRPPISSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIANS-1120334; University 2030; Scott AN.J., McWulty 1, Todd D.; Characterisation of a chicken anaemia virus variant population that resists neutralisation with a group-specific monoclonal antibody."; Arch. virol. 146:713-728(201).

EMBL; AJ297683; CAC14761.1; -.

EMBL; AJ297689; CAC14751.1; -.

EMBL; AJ297689; CAC14751.1; -.

EMBL; AJ297689; CAC14752.1; -.

EMBL; AJ297689; CAC14752.1; -.

EMBL; AJ297689; CAC14752.1; -.

EMBL; PSP06888; CAV. VP3.

InterPro; IPR068888; CAV. VP3.

Pfam; PF04771; CAV VP3.

EMBL; AJ272 MW; 33EFA7D7CA93013F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
   Gaps
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.7%; Score 624; DB 2; Length 121; 99.2%; Pred. No. 4e-51; cive 0; Mismatches 1; Indels
1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
NCBI_TaxID=12618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
NCBI_TaxID=12618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AA
```

```
"Pathogenicity, sequence and phylogenetic analysis of Malaysian
Chicken anaemia virus obtained after low and high passages in MSB-1
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Spackman E., Rosenberger J.K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                       Spackman E., Rosenberger J.K.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kono Y.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        He C.Q., Li Y.L.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENBL; AF312310;
ENBL; AF31268; AAK54291;
ENBL; AF4759038; AAL998961;
ENBL; AF475908; AAL79914.1;
ENBL; AF520788; AAM75347.1;
ENBL; AF520788; AAM75347.1;
ENBL; AF520788; PAM75347.1;
ENBL; AF520788; PAM75347.1;
ENBL; AF520788; PAM75347.1;
ENBL; AF520788; PAM7547.1;
ENBL; AF520788; ENDRECTION of apoptosis by virus; IEA.
INTERPROF | ENROGSES | CAV VP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF04771; CAV VP3; Ī.
SEQUENCE 121 AA; 13245 MW; D2AAB39C2BD61A3E CRC64;
                                                                       Arch. Virol. 148:2437-2448(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avian Pathni. 29:305-310(2000).
EMBL, AF311900; AAK70849.2; -.
EMBL, AAB046587; BAB19636.1; -.
EMBL, AB046589; BAB19639.1; -.
EMBL; AB046589; BAB19639.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.2%;
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB046590; BAB19645.1
EMBL; AF199501; AAF08299.1
EMBL; AF285882; AAX83007.1
EMBL; AF313470; AAG34178.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reaction.";
       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TADNSESTGFKNVPDLRIDQPKPPSKKRSCDPSEYRVSELKESLITITTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TADNSESTGFKNVQDLRTDQPKPPSKKRSCDPSEXRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNALQEDTPFGESTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                   MEDINE-2126594. PubMed=11402858;
Scott A.N.J., McNulty M.S., Todd D.;
Characterisation of a chicken anaemia virus variant population that resists neutralisation of a chicken anaemia virus variant population that Arch. Virol. 146:713-728(2001).
EMBL, AJ297681; CAC14755.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0019051; P:induction of apoptosis by virus; IEA.
InterPro; IPR006858; CAV VP3.
EFEM; PRO4771; CAV VP3.
SEQÜENCE 121 AA; 13329 MW, A471DFF69BD61A3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-AH9410;
MEDLINE-21195622; PubMed=11297698;
Yamaguchi S., Imada T., Kaji N., Mase M., Tsukamoto K., Tanimura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yuasa N.;
"Idėntification of a genetic determinant of pathogenicity in chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=14648297;
Chowdhury S.M., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
Md-Zain B.M., Kono Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=21310375; PubMed=11417817;
Van (Santen V.L., Li L., Hoerr F.J., Lauerman L.H.;
"Genetic characterization of chicken anemia virus from commercial broiler chickens in Alabama.";
Avian Dis. 45:373-388 (2001).
                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                     tch 98.7%; Score 624; DB 2; Length 121; sal Similarity 99.2%; Pred. No. 4e-51; 120; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L21 |
SEQUENCE FROM N.A.
van Santen V.L., Toro H., Hoerr F.J.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
NCBI_TaxID=12618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anaemia virus.";
J. Gen. Virol. 82:1233-1238(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q91N81;
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
05-UUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Delrose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wu Z.Q., Li G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=VP3;
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                Best Local
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91N81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q91N81
SORRETTARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       名
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCOCCOS ON THE SERVICE OF THE SERVI
```

```
61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRCIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
SEQUENCE FROM N.A. Chowdiny S.M., Jani I., Hair-Bejo M., Jamaluddin A.A., Chowdhury S.M.Z.H., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A., Kono Y., Darus A.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Chowdhury S.M.Z.H., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNALQEDIPPGPSTVFRPPISSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quantitation of chicken anemia virus by competitive polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Namakkal-Indian;
Jadhao S.J., Pattnaik B., Toshniwal R.M., Dash B.B., Pradhan H.K.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 624; DB 2; Length 121;
Pred. No. 4e-51;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamaguchi S., Kaji N., Munangandu H.M., Kojima C., Mase M.,
Tsukamoto K.;
```

RESULT 9

SO DE REPRESENTATION DE LA PROPERCION DE

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                        61 TADNSESTGFKAVPDLRIDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                            TADNSESTGFKNVPDLRTDQPKPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRCIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TADNSESTGFKOVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA 60
                                                    MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNALOEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                  ö
                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=TR20;
Okamura H., Sakaguchi M., Tokunaga E.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AR027470; BAA77831.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0019951; P:induction of apoptosis by virus; IEA.
InterPro; IPRO06859; CAV VP3.
SEQUENCE 121 AA; 13272 MW; 72B7AE9C2BD60BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                              Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.3%; Score 621; DB 2;
98.3%; Pred. No. 7.6e-51;
iive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=VP3;
Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
98.3%; Pred. No. 7.6e-51;
                                                                                                                                                                                                                                                                                                                           121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AA
                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2003 (TrEMBLrel. 24,
                Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 98.3
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=12618;
                                                                                                                                                                                             121 Ļ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 L 121
                                                                                                                                                                                                                                 i 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VP3 protein.
                                                                                                                                                           61
                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                           Q9WB33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9DWW8
                                                                                                                                                                                                                                                                                   RESULT 11
Q9WB33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OS CY
                                                                                    셤
                                                                                                                                                      ద
                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                    ሯ
                                                                                                                        ઠે
                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TADNSESTGFKNVPDLATDQHKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Chowdhury S.M.Z.H., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                   "Pathogenicity, sequence and phylogenetic analysis of Malaysian Chicken anaemia virus obtained after low and high passages in MSB-1
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
PubMed=14648297;
Chowdhury S.M., Omar A.R., Aini I., Hair-Bejo M., Jamaluddin A.A.,
Md-Zain B.M., Kono Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.6%; Score 623; DB 2; Length 121; 99.2%; Pred. No. 4.9e-51; Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.3%; Score 621; DB 2; Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Kono Y.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AYG01321; AAK82947.1; GO, GO:0014025; C:host cell nucleus; IEA. GO; GO:0019051; P:induction of apoptosis by virus; IEA. InterPro; IPR006859; GAV, VP3. InterPro; IPR06859; GAV, VP3. Fam; PF04771; CAY VP3; I. SEQUENCE 121 AA; 13338 WW; CD34CA7E9BD61A3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=G6;
Imai K., Yamaguchi S.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AB119448; BAD12197.1; -.
InterPro; IRR006858; CAV VP3.
Pfam; PF04771; CAV VP3; I.
SEQUENCE 121 AA; 13272 MW; DA0822253B28FADO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q75ZP9;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                             01-007-7.
01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-00T-2003 (TrEMBLrel. 24, Last senotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VP3.
Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
NCBL_TaxID=12618;
                                                                                                                                                                        Chicken anemia virus. .
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
VGBI_TaxID=12618;
                                                                     121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 AA.
                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                       cells.";
Arch. Virol. 148:2437-2448(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.2<sup>3</sup>
Matches 120; Conservative
                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0752F9
                                                                 QBJNK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
Q752F9
```

셤

ઠ 셤

ઠે 셤 ઠે AC OOC OOR BELL RELEASED BY AC OOC OOK OOK RELEASED BY RELEASED BY

SECUENCE

Query Match

ò g à

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TADNSESTGFKAVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTPSRPRTARRCIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNGLQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNALOEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                MEDLINE=21310375; PubMed=11417817; van Santen V.L., Li L., Hoerr P.J., Lauerman L.H.; van Santen V.L., Li L., Hoerr P.J., Lauerman L.H.; Genetic characterization of chicken anemia virus from commercial broiler chickens in Alabama."; Ayian Dis. 45:373-388 (2001).
                                                                                                                                                                                                                                               P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

A van Santen V.L., Toro H., Hoerr F.J.;

L submitted (UUL-2003) to the EMBL/GenBank/DDBJ databases.

St. Submitted (UUL-2003) to the EMBL/GenBank/DDBJ databases.

B EMBL; AF311892; AAK70825.2; -..

C GO: GO::0019026; C::nost cell nucleus; IEA.

DR GO; GO::0019051; P::niduction of apoptosis by virus; IEA.

DR GO; GO::0019051; P::niduction of apoptosis by virus; IEA.

DR Heam; PF04771; CAV_VP3;

DR Pfam; PF04771; CAV_VP3;

SEQUENCE 121 AA; 13231 MW; B4AAB39C2DD618AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          98.1%; Score 620; DB 2; Length 121; 98.3%; Pred. No. 9.5e-51; rive 0; Mismatches 2; Indels
                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptin (VP3).
Chicken anemia virus (Japanese isolate 82-2) (CAV)
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
                                                                      Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AA
   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006858; CAV_VP3.
   25, 1
26, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D31965; BAA06733.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 98.3 Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                            FROM N.A.
                                                                                                       NCBI_TaxID=12618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=73476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996
01-OCT-1996
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VP3 CAV82
P54096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
VP3_CAV82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TADNSESTGFKNVPDLRTDQPKPPSKKRSCDPSEYRVSELKESLITTTPSRPRTARRIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                1 MNALQEDTPPGPSTVFRPPTSSRPLETPHCREIRIGIAGITITLSLCGCANARAPTLRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNALQEDTPPGPSTVPRPPTSSRPLETPHCREIRIGIAGITILSLCGCANARAPTLRSA
           ٤
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                          Scott A.N.J., McNulty M.S., Todd D.;
"Characterisation of a chicken anaemia virus variant population that
"Characterisation of a chicken anaemia virus variant population that
aresists neutrallsation with a group-specific monoclonal antibody.";
Arch. Virol. 146:713-728(2001).
EMBL, AJ297666; CAC14770.1;
GO: GO: GO: 0042025; C: host cell nucleus; IEA.
GO: GO: GO: 0019051; P: induction of apoptosis by virus; IEA.
InterPro; PRE006658; CAV VP3.
Pfam: PPC04771; CAV VP3.
EEGUENCE 121 AA; 13240 MW; D7ABB05D37A61A3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Imai K., Yamaguchi S.;
"Autigenic variation among Chicken anemia virus strains.";
"Autigenic variation among Chicken anemia virus strains.";
Expunitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; ABJ19448; BAJ12197.1; -.
SEQUENCE 121 AA; 13272 MW; DA0822253B28FADO CRC64;
                                                                                                                                                                                                                                                                       Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                     Score 621; DB 2; Length 12
Pred. No. 7.6e-51;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 621; DB 2;
Pred. No. 7.6e-51;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicken anemia virus.
Viruses; ssDNA viruses; Circoviridae; Gyrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                           MEDLINE=21296594; PubMed=11402858;
                                                                                                                                                                                                                                                                         98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.3%;
98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-2004 (TrEMBLrel. 27, 10-MAR-2004 (TrEMBLrel. 27, 10-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 119; Conservative
                                                                                                                                                                                                                                                                                       Best Local Similarity 98.3
Matches 119, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=12618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=G6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
```

BAD12197 BAD12197

RESULT 13 BAD12197

셤

ö

셤

Query Match

a à 셤 ð

ð

Q91NA5 Q91NA5;

RESULT Q91NA5

9 9

Gaps

; 0

j

```
DR Pfam; PF04771; CAV_VP3; 1.

KW Apoptosis; Nuclear protein.

SQ SEQUENCE 121 AA; 13233 MW; C770839C2BD61A3E CRC64;

Query Macry Mathematical Capacity of 34; Score 619; DB 1; Length
```

Query Match

Best Local Similarity 98.3%; Pred. No. 1.2e-50;
Matches 119; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 121 L 121 Db 121 L 121

g

8 8 8

Search completed: December 23, 2004, 11:03:31 Job time : 197 secs

ī.

Mis Pogo Blonk (USDIO)

\_ \_\_\_\_\_